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OM protein - protein search, using sw model

Run on: June 1, 2005, 11:37:44 ; Search time 128.533 Seconds
(without alignments)
24.072 Million cell updates/sec

Title: US-09-424-940A-2

Perfect score: 50

Sequence: 1 GHRPLDKC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Genesecp1980s:*
- 2: Genesecp1990s:*
- 3: Genesecp2000s:*
- 4: Genesecp2001s:*
- 5: Genesecp2002s:*
- 6: Genesecp2003as:*
- 7: Genesecp2003bs:*
- 8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	8	1 AAP82686	Aap82686 Human fib
2	50	100.0	8	2 AAR44837	Aar44837 Human fib
3	50	100.0	8	2 AAR65793	Aar65793 Fibrin-sp
4	50	100.0	8	2 AAR63270	Aar63270 Synthetic
5	41	82.0	7	1 AAP71314	Aap71314 Sequence
6	41	82.0	7	2 AAR05558	Aar05558 Peptide a
7	41	82.0	7	2 AAR65792	Aar65792 Fibrin-sp
8	41	82.0	7	2 AAR63269	Aar63269 Beta-pept
9	41	82.0	9	4 ABB76979	Abb76979 Residues
10	41	82.0	10	2 AAW11931	Aaw11931 Fibrinoge
11	41	82.0	11	7 ADD32229	Add32229 Biotinyla
12	41	82.0	12	2 AAR28629	Aar28629 N-termi
13	41	82.0	12	2 AAR44829	Aar44829 Human fib
14	41	82.0	12	2 AAR44838	Aar44838 Human fib
15	41	82.0	14	5 ABB78036	Abb78036 Peptide w
16	41	82.0	16	2 AAR44830	Aar44830 Human fib
17	41	82.0	20	6 AAE34816	Aae34816 S. epider
18	41	82.0	25	6 AAE34814	Aae34814 S. epider
19	41	82.0	28	2 AAR40010	Aar40010 Scintigra
20	41	82.0	28	2 ADD12888	Add12888 scintigra
21	41	82.0	28	5 AAO18333	Aao18333 Fibrinoge
22	41	82.0	29	2 AAR42547	Aar42547 Leukocyte
23	41	82.0	30	2 AAR42546	Aar42546 Leukocyte
24	41	82.0	30	6 ABP56240	Abp56240 Targeting
25	41	82.0	30	8 ADE64331	Ade64331 Radiophar

26	41	82.0	30	8 ADH58575	Adh58575 Radiophar
27	41	82.0	87	4 ABB11339	Abb11339 Human bet
28	41	82.0	118	3 AAG00151	Aag00151 Human sec
29	41	82.0	140	4 AAU33273	Aau33273 Novel hum
30	41	82.0	141	4 AAO10778	Aao10778 Human pol
31	41	82.0	150	3 AAG00150	Aag00150 Human sec
32	41	82.0	453	4 AAM78493	Aam78493 Human pro
33	41	82.0	455	8 ABM85149	Abm85149 Human dia
34	41	82.0	455	8 ABM85150	Abm85150 Human dia
35	41	82.0	474	8 ABM85152	Abm85152 Human dia
36	41	82.0	474	8 ABM84478	Abm84478 Human dia
37	41	82.0	474	8 ABM84481	Abm84481 Human dia
38	41	82.0	474	8 ABM84482	Abm84482 Human dia
39	41	82.0	474	8 ABM85151	Abm85151 Human dia
40	41	82.0	488	8 ADE76868	Ade76868 Human pro
41	41	82.0	491	2 AAR82243	Aar82243 Human fib
42	41	82.0	491	4 AAM78492	Aam78492 Human pro
43	41	82.0	491	6 AAE36413	Aae36413 Human FBG
44	41	82.0	491	7 ADD69271	Add69271 Human fib
45	41	82.0	491	7 ADD69272	Add69272 Human fib

ALIGNMENTS

RESULT 1
AAP82686
ID AAP82686 standard; peptide; 8 AA.

XX AAP82686;
AC
XX
DT 25-MAR-2003 (revised)
DT 05-DEC-1990 (first entry)
XX
DE Human fibrin beta chain N-terminal.
XX
KW Fibrin; beta chain; N-terminal; monoclonal antibody; thrombosis.
XX
OS Synthetic.
XX
PN JP63093800-A.
XX
PD 25-APR-1988.
XX
PF 08-OCT-1986; 86JP-00237876.
XX
PR 08-OCT-1986; 86JP-00237876.
XX
(MITN) MITSUBISHI GAS CHEM CO INC.
XX
WPI; 1988-152086/22.

PT New anti-human fibrin mono:clonal antibody, for diagnosing thrombosis -
PT pred. from hybridoma obtd. by applying cell fusion mouse spleen and
PT mouse myeloma-cells, and measures human fibrin.

XX Claim 1; Page 1; 8pp; Japanese.

PS The peptide is linked to a carrier protein via a linking agent and used
CC to immunise mice. The mouse spleen cells and amveloma cell line can be
CC fused to produce a hybridoma secreting Mabs which bind specifically to
CC human fibrin but not fibrinogen. (Updated on 25-MAR-2003 to correct PA
CC field.)

XX Sequence 8 AA;

Query Match 100.0%; Score 50; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8

DB 1 GHRPLDKC 8

RESULT 2
 AAR44837
 ID AAR44837 standard; peptide; 8 AA.
 XX
 AC AAR44837;
 XX
 DT 20-JUN-1994 (first entry)
 XX
 DE Human fibrin beta-chain N-terminal peptide A.
 XX
 KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin;
 KW monoclonal antibody; Hydrindoma; thrombolytic antithrombotic agent;
 KW bispecific antibody.
 XX
 OS Synthetic.
 XX
 PN JP05304992-A.
 XX
 PD 19-NOV-1993.
 XX
 PF 17-JUN-1992; 92JP-00158301.
 XX
 PR 20-JUN-1991; 91JP-00148936.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX WPI; 1993-408334/51.
 XX
 XX Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug
 PT increased thrombolytic activity and specificity and reduced reactivity to
 PT fibrinogen.
 XX
 XX Example 1; Page 14; 38pp; Japanese.
 XX
 CC Human fibrin beta-chain peptides A and B were synthesised and coupled to
 CC BSA for injection into mice. The peptides were used to raise antibodies
 CC to human fibrin. Monoclonal antibodies specific for fibrin are used in
 CC the production of bispecific monoclonal antibodies which also recognise
 CC truncated tPA muteins lacking the finger, EGF and Kringle 1 domains
 XX
 XX Sequence 8 AA;
 Query Match 100.0%; Score 50; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDKC 8
 DB |||||
 1 GHRPLDKC 8
 RESULT 3
 AAR65793
 ID AAR65793 standard; peptide; 8 AA.
 XX
 AC AAR65793;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-JUN-1995 (first entry)
 XX
 DE Fibrin-specific epitopic peptide.
 XX
 KW Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;
 KW antifibrin-specific monoclonal antibodies.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 8
 PT /note= "May be absent and if present may be bonded to
 FT keynote limpet hemocyanin."
 FT

XX US5357042-A.
 PN
 XX 18-OCT-1994.
 PD
 XX 24-AUG-1992; 92US-00932729.
 PF
 XX 23-APR-1984; 84US-00603155.
 PR
 XX 30-JAN-1986; 86US-00824228.
 PR
 XX 22-DEC-1989; 89US-00454954.
 PR
 XX (GEHO) GEN HOSPITAL CORP.
 PA
 XX Hui K, Matsueda CR, Haber E;
 PI WPI; 1994-332411/41.
 XX
 XX Synthetic epitopic peptide(s) of variable length - capable of eliciting
 PT fibrin specific antibodies free of fibrinogen cross-reactivity.
 PT
 XX Claim 3; Col 18; 12pp; English.
 PS
 XX AAR65789-R65794 are synthetic peptides comprising fibrin-specific
 CC epitopic sequences, they can be used to prepare hybridoma cell lines,
 CC which produce antifibrin-specific monoclonal antibodies substantially
 CC devoid of fibrinogen cross-reactivity. These antibodies are useful in the
 CC in vivo and in vitro detection of thrombi and fibrin deposits. (Updated
 CC on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 8 AA;
 Query Match 100.0%; Score 50; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDKC 8
 DB |||||
 1 GHRPLDKC 8
 RESULT 4
 AAR63270
 ID AAR63270 standard; peptide; 8 AA.
 XX
 AC AAR63270;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-JUL-1995 (first entry)
 XX
 DE Synthetic beta-peptide used to raise monoclonal antibody 59D8.
 XX
 KW Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
 KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; p79;
 KW coronary stent implantation; adjunctive therapy; fibrinogen; haemorrhage.
 XX
 OS Synthetic.
 XX
 PN WO9425491-A1.
 XX
 PD 10-NOV-1994.
 XX
 PF 03-MAY-1994; 94WO-US004881.
 XX
 PR 03-MAY-1993; 93US-00058699.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (UYEW-) UNIV EMORY.
 XX
 XX Haber E, Bode C, Runge M;
 PI WPI; 1994-358195/44.
 XX
 XX Fibrin-binding antibody linked to thrombin inhibitor - useful for
 PT

PT preventing blood coagulation by specifically targetting inhibitor to site
 PT of thrombin activity.

XX Example 1; Page 14; 53pp; English.

XX This sequence represents a synthetic beta-peptide which was used to
 CC immunopurify the monoclonal antibody 5908 which was raised against beta-
 CC peptide (see also AAR63269). The antibody binds fibrin and may be used in
 CC the chimeric molecule of the invention. The chimeric molecule further
 CC comprises a thrombin inhibitor linked to the fibrin-binding antibody
 CC through a covalent linkage. The chimeric molecule allows fibrin-specific
 CC antibody targetting of hirudin and other thrombin inhibitors, which is
 CC more potent than thrombin on its own. The epitope to which 5908 binds
 CC becomes available only after thrombin cleaves fibrinopeptide B. The
 CC chimeric protein may be used for preventing coagulation of the blood.
 CC Anti-thrombin targetting can be esp. useful in highly thrombogenic
 CC situations such as coronary stent implantation and can be used as an
 CC adjunctive therapy with highly selective thrombolytic agents. The
 CC thrombin inhibitor is localised to sites of thrombin activity by the
 CC antibody which binds to thrombin but does not cross react with uncleaved
 CC fibrinogen. The selectivity of inhibition allows the total amount of
 CC thrombin inhibitor used to be substantially reduced, resulting in a
 CC reduced potential for generalised haemorrhaging. (Updated on 25-MAR-2003
 CC to correct PN field.)

XX Sequence 8 AA;

Query Match 100.0%; Score 50; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
 Db 1 GHRPLDKC 8

RESULT 5

AAP71314
 ID AAP71314 standard; peptide; 7 AA.

XX AAP71314;

XX 25-MAR-2003 (revised)
 DT 03-OCT-2002 (revised)
 DT 19-JUN-1991 (first entry)

XX Sequence of fibrin immunogen for the prepn. of monoclonal antibodies
 DE (Wabs).

XX Fibrin-specific monoclonal antibody; screening.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 7 /label= Lys-OH

XX W08706263-A.

XX 22-OCT-1987.

XX 14-APR-1987; 87WO-US000862.

XX 14-APR-1986; 86US-00851514.

XX (GEO) GEN HOSPITAL CORP.

PA (GEO) GEN HOSPITAL CORP.

PA (GEO) GEN HOSPITAL CORP.

XX Matsueda GR, Haber E;

XX WPI; 1987-306855/43.

XX

PT Screening of fibrin-specific monoclonal antibodies - by contact with
 PT immobilised crosslinked fibrin clot and screening with detectable
 PT labelling step.

XX Disclosure; Page 7; 41pp; English.

XX The Mabs are specific to fibrin without fibrinogen cross-reactivity. They
 CC have increased binding to in vitro and in vivo thrombi. The Mabs can be
 CC used in immunoassays for fibrin in the presence of fibrinogen or other
 CC proteins. They can be used as immunoaffinity ligands for the purification
 CC of fibrin. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on
 CC 25-MAR-2003 to correct PA field.)

XX Sequence 7 AA;

Query Match 82.0%; Score 41; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 1 GHRPLDK 7

RESULT 6

AAR05558
 ID AAR05558 standard; peptide; 7 AA.

XX AAR05558;

XX 25-MAR-2003 (revised)

DT 11-OCT-1990 (first entry)

XX Peptide antigenic to fibrin.

XX fibrin; fibrinogen; thrombi; immunoaffinity.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 2 /label= His or Pro

FT Misc-difference 4 /label= Pro or Val

FT Misc-difference 5 /label= Leu or Val

FT Misc-difference 6 /label= Asp or Glu

FT Misc-difference 7 /label= Lys or Arg

XX US4927916-A.

XX 22-MAY-1990.

XX 30-JAN-1986; 86US-00824228.

XX 23-APR-1984; 84US-00603155.

XX (GEO) GEN HOSPITAL CORP.

XX Matsueda BR, Haber E, Hui K;

XX WPI; 1990-185723/24.

XX Fibrin-specific monoclonal antibodies - lacking fibrinogen cross-

PT reactivity, obtd. using peptide(s) comprising fibrin-specific epitopic

PT sequences.

XX Claim 1; Page 17; 12pp; English.

XX Peptide is epitopic to fibrin, allowing anti-fibrin Abs to be raised

XX without cross-reactivity to fibrinogen. They are particularly useful in

CC detection of fibrin and thrombi. (Updated on 25-MAR-2003 to correct PA
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 7 AA;

Query Match 82.0%; Score 41; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 |||||
 Db 1 GHRPLDK 7

RESULT 7

AAR65792
 ID AAR65792 standard; peptide; 7 AA.

XX AAR65792;

AC 25-MAR-2003 (revised)

DT 26-JUN-1995 (first entry)

DE Fibrin-specific epitopic peptide.

XX Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;
 KW antifibrin-specific monoclonal antibodies.

XX Synthetic.

PN US357042-A.

XX 18-OCT-1994.

XX 24-AUG-1992; 92US-00932729.

XX 23-APR-1984; 84US-00603155.

PR 30-JAN-1986; 86US-00824228.

PR 22-DEC-1989; 89US-00454954.

XX (GEHO) GEN HOSPITAL CORP.

XX Hui K, Matsueda GR, Haber E;

XX WPI; 1994-332411/41.

XX Synthetic epitopic peptide(s) of variable length - capable of eliciting

PT fibrin specific antibodies free of fibrinogen cross-reactivity.

XX Claim 2; Col 18; 12pp; English.

PS AAR65789-R65794 are synthetic peptides comprising fibrin-specific
 CC epitopic sequences, they can be used to prepare hybridoma cell lines,
 CC which produce antifibrin-specific monoclonal antibodies substantially
 CC devoid of fibrinogen cross-reactivity. These antibodies are useful in the
 CC in vivo and in vitro detection of thrombi and fibrin deposits. (Updated
 CC on 25-MAR-2003 to correct PF field.)

XX Sequence 7 AA;

Query Match 82.0%; Score 41; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 |||||
 Db 1 GHRPLDK 7

RESULT 8

AAR63269
 ID AAR63269 standard; peptide; 7 AA.

XX

AC AAR63269;

XX 25-MAR-2003 (revised)

DT 21-JUL-1995 (first entry)

DE Beta-peptide used to raise monoclonal antibody 59D8.

XX Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;

KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; p79;

KW coronary stent implantation; adjunctive therapy; fibrinogen; haemorrhage.

XX Synthetic.

OS W09425491-A1.

PN 10-NOV-1994.

XX 03-MAY-1994; 94WO-US004881.

XX 03-MAY-1993; 93US-00058699.

PR (HARD) HARVARD COLLEGE.

PA (UYEM-) UNIV EMORY.

XX Haber E, Bode C, Runge M;

XX WPI; 1994-358195/44.

XX Fibrin-binding antibody linked to thrombin inhibitor - useful for
 PT preventing blood coagulation by specifically targetting inhibitor to site
 PT of thrombin activity.
 PS Example 1; Page 13; 53pp; English.
 XX This sequence represents beta-peptide which was used to raise the
 CC monoclonal antibody 59D8. The antibody binds fibrin and may be used in
 CC the chimeric molecule of the invention. The chimeric molecule further
 CC comprises a thrombin inhibitor linked to the fibrin-binding antibody
 CC through a covalent linkage. The chimeric molecule allows fibrin-specific
 CC antibody targetting of hirudin and other thrombin inhibitors, which is
 CC more potent than thrombin on its own. The epitope to which 59D8 binds
 CC becomes available only after thrombin cleaves fibrinopeptide B. The
 CC chimeric protein may be used for preventing coagulation of the blood.
 CC Anti-thrombin targetting can be esp. useful in highly thrombogenic
 CC situations such as coronary stent implantation and can be used as an
 CC adjunctive therapy with highly selective thrombolytic agents. The
 CC thrombin inhibitor is localised to sites of thrombin activity by the
 CC antibody which binds to thrombin but does not cross react with uncleaved
 CC fibrinogen. The selectivity of inhibition allows the total amount of
 CC thrombin inhibitor used to be substantially reduced, resulting in a
 CC reduced potential for generalised haemorrhaging. (Updated on 25-MAR-2003
 CC to correct PN field.)

XX Sequence 7 AA;

QY Query Match 82.0%; Score 41; DB 2; Length 7;
 Db Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 GHRPLDK 7
 |||||
 Db 1 GHRPLDK 7

RESULT 9

ABB76979
 ID ABB76979 standard; peptide; 9 AA.

XX ABB76979;

XX 22-JUL-2002 (first entry)

DE Residues 45-54 of human fibrinogen beta chain precursor.

XX Anti-arthritis; anti-inflammatory; fibrin; rheumatoid polyarthritis;
 KW human; fibrinogen beta chain.
 XX Homo sapiens.
 XX FR2795735-A1.
 XX
 XX 05-JAN-2001.
 XX
 XX 01-JUL-1999; 99FR-00008470.
 XX
 XX 01-JUL-1999; 99FR-00008470.
 XX (UYTO-) UNIV TOULOUSE SABATIER PAUL.
 XX Serre G, Sebbag M;
 PI WPI; 2001-114394/13.
 XX
 XX New citrulline-containing polypeptide from fibrin, useful for diagnosis
 PT and treatment of rheumatoid polyarthritis.
 PT
 XX Example 1; Page 12; 23pp; French.
 XX
 XX The present invention relates to a citrulline (Cit) containing
 CC polypeptide derived from all or part of the alpha- or beta-chains of
 CC fibrin by substitution of at least one arginine residue by Cit. The Cit
 CC containing polypeptides can be used for in vitro diagnosis of rheumatoid
 CC polyarthritis (RP), by detecting disease-specific autoantibodies, and
 CC therapeutically for neutralising the RP-associated autoimmune response.
 CC The present sequence is a fragment (residues 45-54) of the human
 CC fibrinogen beta chain precursor, which was used in an example from the
 CC invention
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 82.0%; Score 41; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db |||||
 1 GHRPLDK 7
 RESULT 10
 AAW11931
 ID AAW11931 standard; peptide; 10 AA.
 XX
 XX AAW11931;
 AC
 XX 02-APR-1997 (first entry)
 XX
 XX Fibrinogen A-alpha-chain residues 17-26.
 XX
 XX Monoclonal; antibody; human; soluble; fibrin; fibrinogen; urea-treated;
 KW des-AABB; A-alpha-chain; immunoassay; diagnosis;
 KW disseminated intravascular coagulation.
 XX
 XX Homo sapiens.
 XX
 XX WO9512617-A1.
 XX
 XX 11-MAY-1995.
 XX
 XX 01-NOV-1994; 94WO-JP001844.
 XX
 XX 02-NOV-1993; 93JP-00297325.
 XX (IATR) IATRON LAB INC.
 XX
 XX Soe G, Kohno I, Inuzuka K, Ito Y;
 PI
 WPI; 1995-206667/27.
 XX Monoclonal antibody reactive with soluble human fibrin - but not with
 PT fibrinogen, is useful for fibrin immunoassay in plasma specimens.
 XX
 XX Example 3; Page 15; 32pp; Japanese.
 XX
 XX A novel monoclonal antibody (MAB) reacts with human soluble fibrin, but
 CC not with human fibrinogen. Specifically when the MAB reacts with urea-
 CC treated des-AABB fibrin the reaction is not inhibited by peptides
 CC corresponding to fibrinogen A-alpha-chain residues 17-26 (AAW11931), B-
 CC beta-chain residues 15-24 (AAW11932) or gamma-chain residues 312-324
 CC (AAW11933). The MAB is useful in immunoassays for soluble fibrin in
 CC plasma samples (e.g. by sandwich immunoassay), particularly for the
 CC diagnosis of pathological conditions such as disseminated intravascular
 CC coagulation
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 82.0%; Score 41; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db |||||
 1 GHRPLDK 7
 RESULT 11
 ADD32229
 ID ADD32229 standard; peptide; 11 AA.
 XX
 XX ADD32229;
 AC
 XX 15-JAN-2004 (first entry)
 XX
 XX Biotinylated fibrin polymerisation associated control peptide.
 DE
 XX anti-rheumatic; anti-inflammatory; antiarthritic; peptide therapy;
 KW proinflammatory; tetrapeptide; inflammation; synovial joint inflammation;
 KW rheumatoid arthritis; fibrinogen A alpha chain; fibrin polymerisation;
 KW human.
 KW
 XX Synthetic.
 OS
 XX US2003109431-A1.
 PN
 XX 12-JUN-2003.
 PD
 XX 17-AUG-2001; 2001US-00931009.
 PF
 XX 17-AUG-2001; 2001US-00931009.
 PR
 XX (SMIT/) SMITH T H.
 PA
 XX Smith TH;
 PI
 XX WPI; 2003-829401/77.
 DR
 XX Inducing proinflammatory effects in human synovial or fibroblast cells
 PT comprises using a specific tetrapeptide which can also identify a
 PT receptor to the tetrapeptide.
 PT
 XX Disclosure; Page 5; 16pp; English.
 PS
 XX The invention describes a method of inducing proinflammatory effects in
 CC synovial or fibroblast cells comprising exposing the cells to a specific
 CC tetrapeptide (GRRP) peptide (I). (I) is used for inducing proinflammatory
 CC effects in synovial or fibroblast cells. An analogue of (I) is used for
 CC treating or preventing inflammation of a synovial joint or rheumatoid
 CC arthritis in a subject. (I) is used to identify a receptor for (I)
 CC comprising exposing several fibroblastic cells or synovial cells to (I).

CC (1) Can identify, isolate and clone the cell receptor to which it binds.
CC This is the amino acid sequence of a control peptide associated with the
CC inhibition of fibrin polymerisation.

XX
SQ Sequence 11 AA;

Query Match 82.0%; Score 41; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||||
Db 1 GHRPLDK 7

RESULT 12

AAR28629
ID AAR28629 standard; peptide; 12 AA.

AC AAR28629;

XX 25-MAR-2003 (revised)

DT 22-MAR-1993 (first entry)

XX N-terminal human fibrin peptide.

XX bispecific hybrid monoclonal antibody; thrombolytic agent;
KW cardiac infarction; arterial embolism; cerebral infarction;
KW peripheral arterial/venous obstruction; retinal arterial obstruction.

XX Homo sapiens.

OS
XX
PN EP513778-A2.

XX
PD 19-NOV-1992.

XX
PF 14-MAY-1992; 92EP-00108134.

XX
PR 17-MAY-1991; 91JP-00112874.

XX
PR 13-MAR-1992; 92JP-00055025.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Iwasa S, Kurokawa T, Watanabe A;

XX WPI; 1992-383677/47.

XX Bi-specific antibody useful for treating thrombotic obstructive diseases
PT e.g. cardiac infarction - comprises antithrombus antibody variable region
PT and anti-thrombolytic substance antibody variable region with no heavy
PT chain constant region domains 2 and 3.

XX Disclosure; Page 3; 30pp; English.

XX This sequence represents an N-terminal peptide of human fibrin. It was
CC used in the production of bispecific monoclonal antibodies which are
CC specific for fibrins, but do not bind fibrinogen, and are specific
CC for anti-thrombolytic substance. The compen. contg. these Abs lacks the
CC side effects of prior art Ab targetted thrombolytic agents and has
CC enhanced thrombolytic activity. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX Sequence 12 AA;

Query Match 82.0%; Score 41; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||||
Db 1 GHRPLDK 7

RESULT 13

AAR44829
ID AAR44829 standard; peptide; 12 AA.

XX
AC AAR44829;

XX 20-JUN-1994 (first entry)

XX Human fibrin beta-chain N-terminal peptide (1-11)-Cys.

KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin;
KW monoclonal antibody; hybridoma; thrombolysis antithrombotic agent;
KW bispecific antibody.

XX Synthetic.

XX Location/Qualifiers

PH Key

FT Region

FT 1..11 /note= "human fibrin beta-chain residues 1-11"

FT Modified-site 12

FT /note= "BSA carrier is attached to Cys"

XX JP05304992-A.

XX 19-NOV-1993.

XX 17-JUN-1992; 92JP-00158301.

XX 20-JUN-1991; 91JP-00148936.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 1993-408334/51.

XX Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug
PT increased thrombolytic activity and specificity and reduced reactivity to
PT fibrinogen.

XX Disclosure; Page 9; 38pp; Japanese.

XX Human fibrin beta-chain N-terminal peptide (1-11)-Cys was synthesised and
CC coupled to BSA for injection into mice. The peptide was used to raise
CC antibodies to human fibrin. Monoclonal antibodies specific for fibrin are
CC used in the production of bispecific monoclonal antibodies which also
CC recognise truncated tPA muteins lacking the finger, EGF and Kringle 1
CC domains

XX Sequence 12 AA;

Query Match 82.0%; Score 41; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||||
Db 1 GHRPLDK 7

RESULT 14

AAR44838
ID AAR44838 standard; peptide; 12 AA.

XX
AC AAR44838;

XX 20-JUN-1994 (first entry)

XX Human fibrin beta-chain peptide B.

KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin;
KW monoclonal antibody; hybridoma; thrombolysis antithrombotic agent;
KW bispecific antibody.

XX Synthetic.

XX JP05304992-A.
XX 19-NOV-1993.
XX 17-JUN-1992; 92JP-00158301.
XX 20-JUN-1991; 91JP-00148936.
XX (TAKE) TAKEDA CHEM IND LTD.
XX WPI; 1993-408334/51.
XX Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug
XX increased thrombolytic activity and specificity and reduced reactivity to
XX fibrinogen.
XX Example 1; Page 14; 38pp; Japanese.
XX Human fibrin beta-chain peptides A and B were synthesised and coupled to
XX BSA for injection into mice. The peptides were used to raise antibodies
XX to human fibrin. Monoclonal antibodies specific for fibrin are used in
XX the production of bispecific monoclonal antibodies which also recognise
XX truncated tPA muteins lacking the finger, EGF and Kringle 1 domains
XX Sequence 12 AA;
Query Match 82.0%; Score 41; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
DB 6 GHRPLDK 12
RESULT 15
ABB78036
ID ABB78036 standard; peptide; 14 AA.
XX AC ABB78036;
XX DT 22-OCT-2002 (first entry)
XX DE Peptide WTM250 derived from fibrin/fibrinogen beta chain.
XX KW Fibrin beta chain; fibrinogen beta chain; fibrin fragment E;
XX cell proliferation; angiogenesis; fibrogenesis; collagen synthesis;
XX wound healing; skin graft; heart muscle revascularisation;
XX limb replacment; ischaemia; scarring; restenosis; atherosclerosis;
XX rheumatoid arthritis; diabetes; renal disease; psoriasis;
XX macular degeneration; cancer; fibrin glue; stent; angioplasty;
XX antenapedia protein; membrane translocation.
XX OS Synthetic.
XX WO200248181-A1.
XX 20-JUN-2002.
XX 12-DEC-2001; 2001WO-GB005505.
XX 12-DEC-2000; 2000GB-00030309.
XX (UYAB-) UNIV ABERDEEN.
XX Melvin WT, Thompson WD, Stirk CM;
XX WPI; 2002-590565/63.
XX Novel peptides acting as modulators of fibrin fragment E activity for
XX treating disease responding to stimulation or inhibition of cell
XX proliferation or angiogenesis e.g. wound healing, ischemia, cancer and

PT psoriasis.
XX Example 3; Page 46; 84pp; English.
XX The specification describes peptides which correspond to portions of
XX fibrin/fibrinogen beta chain sequences, and act as modulators of fibrin
XX fragment E activity, and in turn modulators of fibrin E effects. Such
XX effects include induction of cell proliferation, angiogenesis, wound
XX fibrogenesis and collagen synthesis. The peptides are used for treating
XX heart muscle or limb replacement surgery. They are also used for treating
XX ischaemia, reduction of scarring, and prevention of restenosis. The
XX peptides may also be used for treating atherosclerosis, rheumatoid
XX arthritis, diabetes, renal disease, psoriasis, macular degeneration, or
XX cancer. The peptides are also useful for modifying fibrin glues, and may
XX be incorporated into a stent which is introduced into the arteries of the
XX patient during an angioplasty procedure for preventing restenosis.
XX ABB78036-38 represent peptides derived from fibrin/fibrinogen beta chain
XX sequences. The peptides are derived from the region where plasmin cleaves
XX the molecule, and contain a C-terminal Cys which does not appear in the
XX wild type protein
XX Sequence 14 AA;
Query Match 82.0%; Score 41; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
DB 1 GHRPLDK 7
RESULT 16
AAR44830
ID AAR44830 standard; peptide; 16 AA.
XX AC AAR44830;
XX DT 20-JUN-1994 (first entry)
XX DE Human fibrin beta-chain internal peptide fragment.
XX KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin;
XX monoclonal antibody; hybridoma; thrombolysis antithrombotic agent;
XX bispecific antibody.
XX OS Synthetic.
XX JP05304992-A.
XX 19-NOV-1993.
XX 17-JUN-1992; 92JP-00158301.
XX 20-JUN-1991; 91JP-00148936.
XX (TAKE) TAKEDA CHEM IND LTD.
XX WPI; 1993-408334/51.
XX Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug
XX increased thrombolytic activity and specificity and reduced reactivity to
XX fibrinogen.
XX Disclosure; Page 9; 38pp; Japanese.
XX Human fibrin internal peptide fragment was identified as a candidate
XX immunogen to raise antibodies to human fibrin. Monoclonal antibodies
XX specific for fibrin are used in the production of bispecific monoclonal
XX antibodies which also recognise truncated tPA muteins lacking the finger,
XX EGF and Kringle 1 domains

```

SQ Sequence 16 AA;
Query Match      82.0%; Score 41; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 6 GHRPLDK 12

RESULT 17
AAE34816
ID AAE34816 standard; peptide; 20 AA.
XX AC
XX AAE34816;
XX DT
XX 28-MAY-2003 (first entry)
XX DE
XX S. epidermidis fibrinogen (Fg) Bbeta chain peptide, beta6-25.
XX KW
XX Thrombin-induced blood coagulation; myocardial infarction; SdrG protein;
XX KW sickle-cell crisis; venous thrombosis; stroke; therapy; anticoagulant;
XX KW fibrinogen; Fg.
XX OS
XX Staphylococcus epidermidis.
XX PN WO200292117-A1.
XX PD
XX 21-NOV-2002.
XX PF
XX 13-MAY-2002; 2002WO-US014741.
XX PR
XX 11-MAY-2001; 2001US-0290072P.
XX PA
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI
XX Davis S, Hook MAO;
XX DR WPI; 2003-140257/13.
XX CC
XX Treating or preventing thrombin-induced coagulation of blood for treating
XX PT a disease condition such as stroke, myocardial infarction, sickle-cell
XX PT crisis or venous thrombosis by administering a SdrG protein.
XX PS
XX Example 1; Col 19; 29pp; English.
XX CC
XX The invention relates to a method for treating or preventing thrombin-
XX CC induced coagulation of blood by administering a SdrG protein. The method
XX CC is sued for preparing a composition for treating myocardial infarction,
XX CC stroke, sickle-cell crisis or venous thrombosis. The present sequence is
XX CC Staphylococcus epidermidis fibrinogen (Fg) Bbeta chain peptide used to
XX CC illustrate the method of the invention
XX SX
XX Sequence 20 AA;
Query Match      82.0%; Score 41; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 10 GHRPLDK 16

RESULT 18
AAE34814
ID AAE34814 standard; peptide; 25 AA.
XX AC
XX AAE34814;
XX DT
XX 28-MAY-2003 (first entry)
XX PR
XX 20-APR-1992; 92US-00871282.
XX XX

DE DE
XX KW
XX Thrombin-induced blood coagulation; myocardial infarction; SdrG protein;
XX KW sickle-cell crisis; venous thrombosis; stroke; therapy; anticoagulant;
XX KW fibrinogen; Fg.
XX OS
XX Staphylococcus epidermidis.
XX PN WO200292117-A1.
XX PD
XX 21-NOV-2002.
XX PF
XX 13-MAY-2002; 2002WO-US014741.
XX PR
XX 11-MAY-2001; 2001US-0290072P.
XX PA
XX (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI
XX Davis S, Hook MAO;
XX DR WPI; 2003-140257/13.
XX CC
XX Treating or preventing thrombin-induced coagulation of blood for treating
XX PT a disease condition such as stroke, myocardial infarction, sickle-cell
XX PT crisis or venous thrombosis by administering a SdrG protein.
XX PS
XX Example 1; Col 19; 29pp; English.
XX CC
XX The invention relates to a method for treating or preventing thrombin-
XX CC induced coagulation of blood by administering a SdrG protein. The method
XX CC is sued for preparing a composition for treating myocardial infarction,
XX CC stroke, sickle-cell crisis or venous thrombosis. The present sequence is
XX CC Staphylococcus epidermidis fibrinogen (Fg) Bbeta chain peptide used to
XX CC illustrate the method of the invention
XX SX
XX Sequence 25 AA;
Query Match      82.0%; Score 41; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 15 GHRPLDK 21

RESULT 19
AAE40010
ID AAR40010 standard; peptide; 28 AA.
XX AC
XX AAR40010;
XX DT
XX 25-MAR-2003 (revised)
XX DT 23-MAY-1994 (first entry)
XX DE
XX Scintigraph imaging agent specific binding peptide.
XX KW
XX Reagent; site imaging; technetium-99m labelled; peptide.
XX OS
XX Synthetic.
XX XX
XX Key Location/Qualifiers
XX FT Modified-site 28
XX FT /note= "C-terminal amide"
XX PN WO9321962-A1.
XX XX
XX 11-NOV-1993.
XX PF
XX 19-APR-1993; 93WO-US003687.
XX PR
XX 20-APR-1992; 92US-00871282.
XX XX

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PA (DIAT-) DIATECH INC.
 XX Dean RT, Buttram S, McBride W, Lister-James J, Civitello ER;
 XX WPI; 1993-368429/46.
 DR Reagents for preparing scintigraphic imaging agents - contg. technetium-
 XX 99m labelled peptide(s) contg. 3-100 aminoacid(s).
 PT Claim 35; Page 39; 55pp; English.
 PS The sequence is that of a specific binding peptide used as part of a
 XX reagent for preparing a scintigraphic imaging agent for imaging sites
 CC within a mammalian body. In this the peptide is covalently linked to a
 CC radiolabel-binding moiety which is capable of forming a complex with a
 CC radiolabel, pref. technetium-99m. (Updated on 25-MAR-2003 to correct PN
 CC field.) (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 28 AA;
 Query Match 82.0%; Score 41; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB |||||
 1 GHRPLDK 7

RESULT 20
 ADD12888
 ID ADD12888 standard; peptide; 28 AA.
 XX
 AC ADD12888;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE scintigraphic imaging agent associated peptide #12.
 XX
 XX imaging; scintigraphic imaging agent; SIA; Technetium-99m; tumour;
 KW somatostatin receptor; leukocytes; atherosclerotic plaque;
 KW deep vein thrombosis.
 XX
 OS Synthetic.
 XX
 PN WO9533498-A1.
 XX
 PD 14-DEC-1995.
 XX
 PF 01-JUN-1995; 95WO-US007017.
 XX
 PR 03-JUN-1994; 94US-00253678.
 XX
 PA (DIAT-) DIATECH INC.
 XX
 PI Dean RT, Buttram S, McBride W, Lister-James J, Civitello ER;
 XX WPI; 1996-039983/04.
 DR Scintigraphic imaging agent comprising specific binding peptide -
 PT attached via an amino acid side chain to a radiolabel binding gp.,
 PT provides rapid imaging of tumours, thrombosis etc.
 XX
 PS Claim 14; Page 34; 43pp; English.
 XX
 XX The invention describes a reagent (A) for producing an agent for imaging
 CC sites in a mammal comprising a specific binding peptide (I) of 3-100
 CC amino acids and, covalently linked to the side chain of an amino acid
 CC residue in (I), a radiolabel binding group (II). Also new are (I)
 CC scintigraphic imaging agents (SIA) containing (A) in which (II) is bound
 CC to a radiolabel; (2) kits for preparation of a radiopharmaceutical
 CC comprising (A) and enough reducing agent to label (A) with Technetium-
 CC 99m. Depending on the nature of (I), SIA can be used to image e.g:

CC tumours that express somatostatin receptors; leukocytes; atherosclerotic
 CC plaque; and deep vein thrombosis. Attachment of (II) to a sidechain
 CC avoids any interference with the specific binding properties of (I) and
 CC makes possible derivatisation of cyclic peptides (which are more
 CC resistant to proteolysis). Images may be recorded only a few minutes
 CC after injection of SIA. This is the amino acid sequence of a peptide
 CC associated with the imaging methods of the invention.
 XX
 SQ Sequence 28 AA;
 Query Match 82.0%; Score 41; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB |||||
 1 GHRPLDK 7

RESULT 21
 AA018333
 ID AA018333 standard; peptide; 28 AA.
 XX
 AC AA018333;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE Fibrinogen based therapeutic peptide #9.
 XX
 XX Fibrin; fibrinogen; antagonist; inflammation; autoimmune disease;
 KW rheumatic disease; organ transplantation; arteriosclerosis;
 KW reperfusion trauma; thrombosis; cancer; antiinflammatory; antibacterial;
 KW immunosuppressive; antirheumatic; antiarteriosclerotic; vasotropic;
 KW thrombolytic; anticoagulant; cytostatic; antipsoptic.
 XX
 OS Unidentified.
 XX
 PN WO200248180-A2.
 XX
 PD 20-JUN-2002.
 XX
 PF 07-DEC-2001; 2001WO-AT000387.
 XX
 PR 12-DEC-2000; 2000AT-00002063.
 XX
 PA (FIBR-) FIBREX MEDICAL RES & DEV GMBH.
 XX
 PI Petzelbauer P;
 XX
 XX WPI; 2002-557605/59.
 DR Peptides or proteins based on fibrin or fibrinogen sequences, useful for
 XX combating fibrin-mediated disorders such as inflammation, transplant
 XX rejection, arteriosclerosis and reperfusion damage.
 PS Claim 5; Page 40; 41pp; German.
 XX
 XX The present invention relates to peptides based on the alpha- and beta-
 CC chain sequences of fibrin/fibrinogen, which are capable of acting as
 CC fibrin antagonists. These are used for the therapy of local and
 CC generalised inflammation associated with infection, autoimmune reactions,
 CC rheumatic disease, immune system dysfunction or genetic disease, for the
 CC prevention and treatment of organ transplantation rejection reactions,
 CC arteriosclerosis, reperfusion trauma, thrombotic disease and increased
 CC fibrin deposition associated with aging, or for the transport of other
 CC medicaments to human or animal endothelial cells. They may also be
 CC effective against fibrin-mediated tumour growth, collagenosis or
 CC psoriasis. The present sequence is a peptide of the invention
 XX
 SQ Sequence 28 AA;
 Query Match 82.0%; Score 41; DB 5; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.45;

FH Key Location/Qualifiers
 FT Modified-site 30 /note= "amidated"
 FT XX
 PN WO200260491-A2.
 XX XX
 XX 08-AUG-2002.
 XX XX
 XX 24-OCT-2001; 2001WO-US050423.
 XX XX
 XX 24-OCT-2000; 2000US-00694992.
 PR 24-OCT-2000; 2000US-00695360.
 PR 24-OCT-2000; 2000US-00695494.
 XX XX
 PA (DIAT-) DIATIDE INC.
 XX XX
 XX Cyr JB, Pearson DA;
 PI WPI; 2003-092782/08.
 DR XX
 XX Composition useful for increasing shelf life of diagnostic and
 PT therapeutic radiopharmaceuticals, comprising radiopharmaceutical
 PT precursor and hydrophilic thioether and/or hydrophilic 6-hydroxy-chroman
 PT derivative.
 XX XX
 XX Claim 15; Page 48; 64pp; English.
 XX XX
 CC The present invention describes a composition (C) comprising a
 CC radiopharmaceutical precursor and a stabiliser selected from hydrophilic
 CC thioether (I) and/or hydrophilic 6-hydroxy-chroman derivative (II). Also
 CC described: (1) stabilising a radiopharmaceutical comprising: combining
 CC the radiopharmaceutical precursor with (I) and/or (II) in a container,
 CC and adding a radionuclide to the container; and (2) a kit comprising a
 CC sealed vial containing the radiopharmaceutical precursor, and (I) and/or
 CC (II). (C) can be used to increase the shelf life of diagnostic and
 CC therapeutic radiopharmaceutical precursors in nuclear medicine. The
 CC stabilisers maintain the radiochemical purity of the radiopharmaceutical
 CC to at least 85, preferably at least 90% of the labeled undegraded
 CC radiopharmaceutical. (C) is suitable for stabilising a wide variety of
 CC radiopharmaceuticals. The present sequence represents a specifically
 CC claimed targeting moiety peptide for a composition from the present
 CC invention
 XX XX
 SQ Sequence 30 AA;
 Query Match 82.0%; Score 41; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB |||||
 4 GHRPLDK 10
 RESULT 25
 ADE64331
 ID ADE64331 standard; peptide; 30 AA.
 XX AC ADE64331;
 XX XX
 DT 29-JAN-2004 (first entry)
 XX XX
 DE Radiopharmaceutical composition stabilising hydrophilic thioether #5.
 XX XX
 KW radiopharmaceutical precursor; hydrophilic thioether;
 KW radiopharmaceutical composition; diagnosis; therapy; shelf life;
 KW diagnostic radiopharmaceutical; therapeutic radiopharmaceutical.
 XX OS Synthetic.
 XX XX
 XX Key Location/Qualifiers
 FT Modified-site 30 /note= "C-terminal amide"
 FT XX
 PN US2003103895-A1.
 XX XX
 XX 05-JUN-2003.
 PD XX
 XX 24-APR-2002; 2002US-00131546.
 PF XX
 XX 24-OCT-2000; 2000US-00695494.
 PR 24-OCT-2001; 2001WO-US050423.
 XX XX
 XX (CYRJ/) CYR J E.
 PA (FEAR/) PEARSON D A.
 XX XX
 PI Cyr JB, Pearson DA;
 XX WPI; 2004-040976/04.
 DR XX
 XX Composition used in diagnosis and therapy comprises stabilizing amount of
 PT hydrophilic thioether and radiopharmaceutical precursor or peptide or
 PT benzodiazepine derivative.
 XX XX
 PS Claim 13; SEQ ID NO 5; 19pp; English.
 XX XX
 CC The invention describes a composition comprising a radiopharmaceutical
 CC precursor and a stabilising amount of a hydrophilic thioether. The
 CC composition is useful as stabiliser of radiopharmaceutical compositions
 CC for use in diagnosis and therapy. The composition is particularly useful
 CC for increasing the shelf life of diagnostic or therapeutic
 CC radiopharmaceuticals. This the amino acid sequence of a hydrophilic
 CC thioether used in the method of stabilising radiopharmaceutical
 CC compositions.
 XX XX
 SQ Sequence 30 AA;
 Query Match 82.0%; Score 41; DB 8; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB |||||
 4 GHRPLDK 10
 RESULT 26
 ADH58575
 ID ADH58575 standard; peptide; 30 AA.
 XX AC ADH58575;
 XX XX
 DT 25-MAR-2004 (first entry)
 XX XX
 DE Radiopharmaceutical composition stabilising peptide #5.
 XX XX
 KW radiopharmaceutical precursor; hydrophilic 6-hydroxy-chroman derivative;
 KW stabiliser; radiopharmaceutical composition; diagnosis; therapy;
 KW shelf life.
 XX OS Synthetic.
 XX XX
 XX Key Location/Qualifiers
 FT Modified-site 29 /note= "C-terminal amide"
 FT XX
 PN US2003103895-A1.
 XX XX
 XX 05-JUN-2003.
 PD XX
 XX 24-APR-2002; 2002US-00131546.
 PF XX
 XX 24-OCT-2000; 2000US-00695494.
 PR 24-OCT-2001; 2001WO-US050423.
 XX XX
 XX (CYRJ/) CYR J E.
 PA

PA (PEARSON) PEARSON D A.
 XX
 PT Cyr JE, Pearson DA;
 XX
 DR WPI; 2004-106449/11.
 XX
 PT Compositions, useful as stabilizers, or for increasing shelf life, of
 XX radiopharmaceuticals for use in diagnosis or therapy, comprises
 PT radiopharmaceutical precursor, hydrophilic thioether and hydrophilic 6-
 XX hydroxy-chroman derivative.
 PS Claim 16; SEQ ID NO 5; 17pp; English.
 XX
 CC The invention describes a composition comprising a radiopharmaceutical
 CC precursor and a hydrophilic 6-hydroxy-chroman derivative. The composition
 CC is useful as stabilizers of radiopharmaceutical compositions for use in
 CC diagnosis and therapy. The composition is particularly useful for
 CC increasing the shelf life of diagnostic or therapeutic
 CC radiopharmaceuticals. This is the amino acid sequence of a peptide used
 CC in the stabilisation of radiopharmaceutical compositions.
 XX
 SQ Sequence 30 AA;
 Query Match 82.0%; Score 41; DB 8; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db 4 GHRPLDK 10
 |||||
 RESULT 28
 ABB11339
 ID ABB11339 standard; peptide; 87 AA.
 AC ABB11339;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human beta-fibrinogen homologue, SEQ ID NO:1709.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
 KW antifungal; vulnary; antiulcer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US0003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX WPI; 2001-457740/49.
 DR
 N-PSDB; ABA08583.

XX
 PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 PS Claim 20; Page 167; 1963pp; English.
 XX
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, and hence
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis; cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX
 SQ Sequence 87 AA;
 Query Match 82.0%; Score 41; DB 4; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db 31 GHRPLDK 37
 |||||
 RESULT 28
 AAG00151
 ID AAG00151 standard; protein; 118 AA.
 XX
 AC AAG00151;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein, SEQ ID NO: 4232.
 DE
 XX Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 KW
 XX Homo sapiens.
 OS
 XX EP1033401-A2.
 PN
 XX

PD 06-SEP-2000.
 XX
 PP 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 DR N-PSDB; AAC00157.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 13; SEQ ID NO 4232; 71pp + Sequence Listing; English.
 CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 SQ Sequence 118 AA;
 Query Match 82.0%; Score 41; DB 3; Length 118;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB 45 GHRPLDK 51
 RESULT 29
 AAU33273
 ID AAU33273 standard; protein; 140 AA.
 AC AAU33273;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #3764.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US008656.
 XX
 PR 18-APR-2000; 2000US-00552929.
 PR 26-JAN-2001; 2001US-00770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 XX
 DR WPI; 2001-514838/56.
 DR N-PSDB; AA190709.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX
 PS Claim 20; SEQ ID NO 24670; 1399pp + Sequence Listing; English.

DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX
 PS Claim 20; Page 752; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 SQ Sequence 140 AA;
 Query Match 82.0%; Score 41; DB 4; Length 140;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB 45 GHRPLDK 51
 RESULT 30
 AA010778
 ID AA010778 standard; protein; 141 AA.
 AC AA010778;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 24670.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US004927.
 XX
 PR 28-FEB-2000; 2000US-00515126.
 PR 18-MAY-2000; 2000US-00577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-514838/56.
 DR N-PSDB; AA190709.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX
 PS Claim 20; SEQ ID NO 24670; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO0010-AAO3910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 141 AA;
Query Match 82.0%; Score 41; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
Db 41 GHRPLDK 47
|||||||
RESULT 31
ID AAG00150 standard; protein; 150 AA.
XX AAG00150;
AC AAG00150;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 4231.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
PI WPI: 2000-500381/45.
DR N-PSDB; AAC00156.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 13; SEQ ID NO 4231; 71pp + Sequence Listing; English.
XX
CC The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from human RNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome

CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX
SQ Sequence 150 AA;
Query Match 82.0%; Score 41; DB 3; Length 150;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
Db 45 GHRPLDK 51
|||||||
RESULT 32
ID AAM78493 standard; protein; 453 AA.
XX AAM78493;
AC AAM78493;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1155.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
DR N-PSDB; AAK51626.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 20; Page 3390-3391; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAW80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication

XX SQ Sequence 453 AA;
Query Match 82.0%; Score 41; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
DB 45 GHRPLDK 51
RESULT 34
ABM85149
ID ABM85149 standard; protein; 455 AA.
XX AC ABM85149;
XX DT 18-NOV-2004 (first entry)
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:5398.
XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX OS Homo sapiens.
XX PN WO2004023973-A2.
XX PD 25-MAR-2004.
XX PF 12-SEP-2003; 2003WO-US028227.
XX PR 12-SEP-2002; 2002US-0410259P.
XX PR 12-SEP-2002; 2002US-0410260P.
XX PA (INCY-) INCYTE CORP.
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patry S, Shi X, Suarez CJ;
XX WPI; 2004-329368/30.
XX DR N-PSDB; ACN43801.
XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX PT in diagnosing a condition, disease or disorder associated with human
XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX PT in gene mapping.
XX PS Claim 27; Page; 190pp; English.
XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
XX CC selected from one of the 2722 sequences defined in the specification. A
XX CC polynucleotide of the invention may have a use in gene therapy. The human
XX CC polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be
XX CC used to diagnose a particular condition, disease or disorder associated
XX CC with human molecules, e.g. cell proliferative disorders,
XX CC autoimmune/inflammatory disorder, developmental disorder, endocrine
XX CC disorder, neurological disorders, gastrointestinal disorders, or
XX CC infections caused by virus, bacteria, fungi or parasite. The dithp
XX CC molecules may also be used in genetic mapping, in identifying individuals
XX CC from minute biological samples, in detecting single nucleotide
XX CC polymorphisms, as molecular weight markers, and for somatic or germline
XX CC gene therapy. The present sequence represents a dithp protein of the
XX CC invention. Note: The sequence data for this patent is not represented in
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 455 AA;
Query Match 82.0%; Score 41; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
DB 45 GHRPLDK 51
RESULT 34
ABM85150
ID ABM85150 standard; protein; 455 AA.
XX AC ABM85150;
XX DT 18-NOV-2004 (first entry)
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:5399.
XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX OS Homo sapiens.
XX PN WO2004023973-A2.
XX PD 25-MAR-2004.
XX PF 12-SEP-2003; 2003WO-US028227.
XX PR 12-SEP-2002; 2002US-0410259P.
XX PR 12-SEP-2002; 2002US-0410260P.
XX PA (INCY-) INCYTE CORP.
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patry S, Shi X, Suarez CJ;
XX WPI; 2004-329368/30.
XX DR N-PSDB; ACN43802.
XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX PT in diagnosing a condition, disease or disorder associated with human
XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX PT in gene mapping.
XX PS Claim 27; Page; 190pp; English.
XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
XX CC selected from one of the 2722 sequences defined in the specification. A
XX CC polynucleotide of the invention may have a use in gene therapy. The human
XX CC polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be
XX CC used to diagnose a particular condition, disease or disorder associated
XX CC with human molecules, e.g. cell proliferative disorders,
XX CC autoimmune/inflammatory disorder, developmental disorder, endocrine
XX CC disorder, neurological disorders, gastrointestinal disorders, or
XX CC infections caused by virus, bacteria, fungi or parasite. The dithp
XX CC molecules may also be used in genetic mapping, in identifying individuals
XX CC from minute biological samples, in detecting single nucleotide
XX CC polymorphisms, as molecular weight markers, and for somatic or germline
XX CC gene therapy. The present sequence represents a dithp protein of the
XX CC invention. Note: The sequence data for this patent is not represented in
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Query Match 82.0%; Score 41; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 45 GHRPLDK 51

RESULT 35

ABM85152
ID ABM85152 standard; protein; 474 AA.

AC ABM85152;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:5401.

XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX Homo sapiens.

XX WO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patry S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

DR N-PSDB; ACN43804.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 474 AA;

SQ

Query Match 82.0%; Score 41; DB 8; Length 474;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 45 GHRPLDK 51

RESULT 36

ABM84478
ID ABM84478 standard; protein; 474 AA.

XX ABM84478;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4727.

XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX Homo sapiens.

XX WO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patry S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

DR N-PSDB; ACN43130.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 474 AA;

Query Match 82.0%; Score 41; DB 8; Length 474;

Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 37.
ABM84481
ID ABM84481 standard; protein; 474 AA.

XX AC ABM84481;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4730.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SU, Elder LV;

PI PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

PI PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

PI PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.
DR N-PSDB; ACN43133.

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX PS Claim 27; Page; 190pp; English.

XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 474 AA;

Query Match 82.0%; Score 41; DB 8; Length 474;
Best Local Similarity 100.0%; Pred. No. 9.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 38
ABM84482
ID ABM84482 standard; protein; 474 AA.

XX AC ABM84482;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4731.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SU, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.
DR N-PSDB; ACN43133.

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX PS Claim 27; Page; 190pp; English.

XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 474 AA;

Query Match 82.0%; Score 41; DB 8; Length 474;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 39

ABM85151
ID ABM85151 standard; protein; 474 AA.

XX AC ABM85151;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:5400.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JB, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Pollicky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;

XX WPI: 2004-329368/30.

XX DR N-PSDB; ACN43803.

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX PS Claim 27; Page; 190pp; English.

XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorders, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIFO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 474 AA;

Query Match 82.0%; Score 41; DB 8; Length 474;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 40

ADE76868
ID ADE76868 standard; protein; 488 AA.

XX AC ADE76868;

XX DT 29-JAN-2004 (first entry)

XX DE Human protein expressed in a liver disorder #11.

XX KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
KW tumour; liver; inflammatory disorder; immune response disorder;
KW high-throughput screening; differential gene expression; gene therapy.

XX OS Homo sapiens.

XX PN US2003108871-A1.

XX PD 12-JUN-2003.

XX PF 30-JUL-2001; 2001US-00919039.

XX PR 28-JUL-2000; 2000US-0222113P.

XX PA (KASE/) KASER M R.

XX PI Kaser MR;

XX WPI: 2004-031227/03.

XX DR N-PSDB; ADE76867.

XX PT Composition comprising several cDNAs that are differentially expressed in
PT treated human C3A liver cell cultures, useful for treating liver
PT disorders.

XX PS Claim 1; SEQ ID NO 33; 41pp; English.

XX CC The invention relates to a composition comprising several cDNAs that are
CC differentially expressed in a liver disorder. The composition is useful
CC for treating liver disorder such as hyperlipidaemia, hypertension, type
CC II diabetes, tumours of the liver and disorders of the inflammatory and
CC immune response. The composition is useful for a high-throughput method
CC of screening several molecules or compounds to identify a ligand which
CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
CC high-throughput method for using a protein to screen several molecules or
CC compounds to identify at least one ligand which specifically binds the
CC protein which involves combining the protein encoded by the cDNA with
CC several of molecules or compounds under conditions to allow specific
CC binding, and detecting specific binding between the protein and a
CC molecule or compound, therefore identifying a ligand which specifically
CC binds the protein. The composition is useful for detecting and
CC quantifying differential gene expression, can be used in gene therapy, to
CC formulate prognosis and to design a treatment regimen and to monitor the
CC efficacy of treatment. The present sequence represents the amino acid
CC sequence of a protein encoded by a cDNA differentially expressed in a
CC liver disorder.

XX SQ Sequence 488 AA;

Query Match 82.0%; Score 41; DB 8; Length 488;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 42 GHRPLDK 48

Search completed: June 1, 2005, 11:48:07
Job time : 128.533 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 11:41:40 ; Search time 32 Seconds
(without alignments)
18.662 Million cell updates/sec

Title: US-09-424-940A-2

Perfect score: 50

Sequence: 1 GHRPLDKC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5A COMB pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB pep.*
5: /cgn2_6/prodata/1/iaa/PTCUS COMB pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	8	1 US-08-058-699-11	Sequence 11, Appl
2	41	82.0	7	1 US-08-058-699-10	Sequence 10, Appl
3	41	82.0	10	2 US-08-448-547-1	Sequence 1, Appl
4	41	82.0	20	4 US-10-142-935-6	Sequence 6, Appl
5	41	82.0	25	4 US-10-142-935-4	Sequence 4, Appl
6	41	82.0	28	1 US-08-486-135-12	Sequence 12, Appl
7	41	82.0	28	1 US-08-470-152-12	Sequence 12, Appl
8	41	82.0	28	2 US-08-468-964B-10	Sequence 10, Appl
9	41	82.0	28	2 US-07-871-282A-10	Sequence 10, Appl
10	41	82.0	28	2 US-08-290-853-33	Sequence 33, Appl
11	41	82.0	28	2 US-08-253-678A-10	Sequence 10, Appl
12	41	82.0	28	3 US-08-582-134B-10	Sequence 10, Appl
13	41	82.0	28	3 US-08-170-299-10	Sequence 10, Appl
14	41	82.0	30	2 US-08-290-853-35	Sequence 35, Appl
15	41	82.0	31	1 US-08-472-535-9	Sequence 9, Appl
16	41	82.0	31	1 US-08-484-774-9	Sequence 9, Appl
17	41	82.0	31	3 US-08-266-178A-9	Sequence 9, Appl
18	41	82.0	118	4 US-09-513-999C-4232	Sequence 4232, Ap
19	41	82.0	150	4 US-09-513-999C-4231	Sequence 4231, Ap
20	41	82.0	488	4 US-09-919-039-33	Sequence 33, Appl
21	41	82.0	451	1 US-08-206-176-4	Sequence 4, Appl
22	41	82.0	493	4 US-09-949-016-9617	Sequence 9617, Ap
23	40	80.0	360	4 US-09-252-991A-18909	Sequence 18909, A
24	37	74.0	177	4 US-09-252-991A-18782	Sequence 18782, A
25	36	72.0	10	4 US-10-142-935-9	Sequence 9, Appl
26	36	72.0	15	4 US-10-142-935-8	Sequence 8, Appl
27	36	72.0	20	4 US-10-142-935-5	Sequence 5, Appl

28	36	72.0	74	4	US-09-248-796A-26425	Sequence 26425, A
29	36	72.0	194	4	US-09-252-991A-23750	Sequence 23750, A
30	35.5	71.0	246	4	US-09-252-991A-21990	Sequence 21990, A
31	35	70.0	155	4	US-09-270-767-39157	Sequence 39157, A
32	35	70.0	155	4	US-09-270-767-54374	Sequence 54374, A
33	35	70.0	1203	4	US-09-799-875-5	Sequence 5, Appl
34	34	68.0	9	3	US-09-258-754-234	Sequence 234, App
35	34	68.0	9	3	US-09-042-107-234	Sequence 234, App
36	34	68.0	9	4	US-09-722-250D-234	Sequence 234, App
37	34	68.0	9	4	US-09-676-765A-234	Sequence 234, App
38	34	68.0	190	4	US-09-248-796A-16727	Sequence 16727, A
39	34	68.0	245	4	US-08-469-260A-38	Sequence 38, Appl
40	34	68.0	245	4	US-08-488-446-38	Sequence 38, Appl
41	34	68.0	245	4	US-08-467-344A-38	Sequence 38, Appl
42	34	68.0	245	4	US-08-424-550B-38	Sequence 38, Appl
43	34	68.0	378	2	US-09-055-097-1	Sequence 1, Appl
44	34	68.0	378	4	US-09-373-902-1	Sequence 1, Appl
45	34	68.0	378	4	US-09-831-630-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-058-699-11
; Sequence 11, Application US/08058699
; Patent No. 5443827
; GENERAL INFORMATION:
; APPLICANT: Edgar Haber
; APPLICANT: Christoph Bode
; APPLICANT: Marschall S. Runge
; TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
; TITLE OF INVENTION: THROMBIN
; NUMBER OF INVENTIONS: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/058,699
; FILING DATE: 19930503
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser, Ph.D.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: Linear
US-08-058-699-11

Query Match 100.0%; Score 50; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 8
| | | | |
Db 1 GHRPLDK 8

RESULT 2

US-08-058-699-10
; Sequence 10, Application US/08058699
; Patent No. 5443827
; GENERAL INFORMATION:
; APPLICANT: Edgar Haber
; APPLICANT: Christoph Bode
; APPLICANT: Marshall S. Runge
; TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/058,699
; FILING DATE: 19930503
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Frazer, Ph.D.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/004001
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: Linear
US-08-058-699-10

Query Match 82.0%; Score 41; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 1 GHRPLDK 7

RESULT 3

US-08-448-547-1
; Sequence 1, Application US/08448547
; Patent No. 5821068
; GENERAL INFORMATION:
; APPLICANT: Soe, Gilbu
; APPLICANT: Kohno, Isao
; APPLICANT: Inuzuka, Kimiko
; APPLICANT: Ito, Yumiko
; TITLE OF INVENTION: ANTI-HUMAN SOLUBLE FIBRIN ANTIBODY,
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,547
; FILING DATE: 30-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01844
; FILING DATE: 01-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-297325
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: Q-38931
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-448-547-1

Query Match 82.0%; Score 41; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 1 GHRPLDK 7

RESULT 4

US-10-142-935-6
; Sequence 6, Application US/10142935
; Patent No. 6835378
; GENERAL INFORMATION:
; APPLICANT: HOOK, Stacey
; APPLICANT: DAVIS, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULANT
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PPT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-6

Query Match 82.0%; Score 41; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |

Db 10 GHRPLDK 16

RESULT 5
US-10-142-935-4
; Sequence 4, Application US/10142935
; Patent No. 6835378
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-4

Query Match 82.0%; Score 41; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 15 GHRPLDK 21

RESULT 6
US-08-486-135-12
; Sequence 12, Application US/08486135
; Patent No. 5720934
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R
; TITLE OF INVENTION: Technetium-99m Labeled peptides for
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,135
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5720934nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,205-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-486-135-12

Query Match 82.0%; Score 41; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 15 GHRPLDK 21

RESULT 7
US-08-470-152-12
; Sequence 12, Application US/08470152
; Patent No. 5780007
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,152
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5780007nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,205-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-470-152-12

Query Match 82.0%; Score 41; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 8
US-08-468-964B-10
; Sequence 10, Application US/08468964B
; Patent No. 5922303
; GENERAL INFORMATION:

; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/468,964B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcdaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: DITI 111D4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (603) 437-8970
; TELEFAX: (603) 437-8977
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-468-964B-10

Query Match 82.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 9
US-07-871-282A-10
; Sequence 10, Application US/07871282A
; Patent No. 5965107
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/07/871,282A
; FILING DATE: 20-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcdaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: DITI 111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (603) 437-8970
; TELEFAX: (603) 437-8977
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-871-282A-10

Query Match 82.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 10
US-08-290-853-33
; Sequence 33, Application US/08290853
; Patent No. 5989519
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging Inflammation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,853
; FILING DATE: 11-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5989519nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,112-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1234
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1

OTHER INFORMATION: /label= BAT
OTHER INFORMATION: /note= "The amino terminus is linked to a BAT
FEATURE: radiolabel binding moiety."
NAME/KEY: Modified-site
LOCATION: 28
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
amide"
US-08-290-853-33

Query Match 82.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 11
US-08-253-678A-10
; Sequence 10, Application US/08253678A
; Patent No. 5997844
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS: 23
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,678A
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: DITI 112
; TELEPHONE: (603) 437-8970
; TELEFAX: (603) 437-8977
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-253-678A-10

Query Match 82.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 12
US-08-582-134B-10
; Sequence 10, Application US/08582134B
; Patent No. 6074627
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS: 23
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,134B
; FILING DATE: 14-MAY-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: DITI 112D1
; TELEPHONE: (603) 437-8970
; TELEFAX: (603) 437-8977
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-582-134B-10

Query Match 82.0%; Score 41; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 13
US-08-170-299-10
; Sequence 10, Application US/08170299
; Patent No. 6086849
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL

; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,299
; FILING DATE: 09-FEB-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6086849nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,205-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-170-299-10

Query Match 82.0%; Score 41; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 14
US-08-290-853-35
; Sequence 35, Application US/08290853
; Patent No. 5989519
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging Inflammation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,853
; FILING DATE: 11-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5989519nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,112-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= Picolinoyl
; OTHER INFORMATION: /note= "The amino terminal residue is
; OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine is
; OTHER INFORMATION: protected by an acetamidomethyl group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 30
; OTHER INFORMATION: /label= Amide
; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
; OTHER INFORMATION: amide"
; US-08-290-853-35

Query Match 82.0%; Score 41; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 3 GHRPLDK 9

RESULT 15
US-08-472-535-9
; Sequence 9, Application US/08472535
; Patent No. 5711931
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lees, Robert S.
; APPLICANT: Buttram, Scott
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging Inflammation
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,535
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5711931nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,112-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= picolinoyl
; OTHER INFORMATION: /note= "The amino terminal residue is

OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine
residue is protected by an acetoamidomethyl

Query Match 82.0%; Score 41; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 4 GHRPLDK 10

RESULT 16

US-08-484-774-9

Sequence 9, Application US/08484774

Patent No. 5807538

GENERAL INFORMATION:

APPLICANT: Dean, Richard T

APPLICANT: Lees, Robert S.

APPLICANT: Buttram, Scott

TITLE OF INVENTION: Technetium-99m Labeled Peptides for

TITLE OF INVENTION: Imaging Inflammation

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,774

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: No. 5807538nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,112-K

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1..3

OTHER INFORMATION: /label= Picolinoyl

OTHER INFORMATION: /note= "The amino terminal residue is

pyridine-2-carbonyl; the thiol of the cysteine

residue is protected by an acetoamidomethyl

US-08-484-774-9

Query Match 82.0%; Score 41; DB 1; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.36;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

Db 4 GHRPLDK 10

RESULT 17

US-08-484-774-9

Sequence 9, Application US/08484774

Patent No. 5807538

GENERAL INFORMATION:

APPLICANT: Dean, Richard T

APPLICANT: Lees, Robert S.

APPLICANT: Buttram, Scott

TITLE OF INVENTION: Technetium-99m Labeled Peptides for

TITLE OF INVENTION: Imaging Inflammation

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,774

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: No. 5807538nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,112-K

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1..3

OTHER INFORMATION: /label= Picolinoyl

OTHER INFORMATION: /note= "The amino terminal residue is

pyridine-2-carbonyl; the thiol of the cysteine

residue is protected by an acetoamidomethyl

US-08-484-774-9

Query Match 82.0%; Score 41; DB 1; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.36;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

Db 4 GHRPLDK 10

RESULT 18

US-09-513-999C-4232

Sequence 4232, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

US-08-266-178A-9

Sequence 9, Application US/08266178A

Patent No. 6017510

GENERAL INFORMATION:

APPLICANT: Dean, Richard T

APPLICANT: Buttram, Scott

TITLE OF INVENTION: Technetium-99m Labeled Peptides for

TITLE OF INVENTION: Imaging Inflammation

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/266,178A

FILING DATE: 27-JUN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 6017510nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,112

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1..3

OTHER INFORMATION: /label= Picolinoyl

OTHER INFORMATION: /note= "The amino terminal residue is

pyridine-2-carbonyl; the thiol of the cysteine

residue is protected by an acetoamidomethyl

US-08-266-178A-9

Query Match 82.0%; Score 41; DB 3; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.36;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

Db 4 GHRPLDK 10

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; SOFTWARE: Patent.pm
; SEQ ID NO 4232
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -30..-1
; OTHER INFORMATION: score 12.2
; OTHER INFORMATION: seq LLLLLLCVFLVKS/QG
US-09-513-999C-4232

Query Match      82.0%; Score 41; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 19
US-09-513-999C-4231
; Sequence 4231, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4231
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -30..-1
; OTHER INFORMATION: score 12.2
; OTHER INFORMATION: seq LLLLLLCVFLVKS/QG
US-09-513-999C-4231

Query Match      82.0%; Score 41; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 20
US-09-919-039-33
; Sequence 33, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 33
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; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 3393861CD1
US-09-919-039-33

Query Match      82.0%; Score 41; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 42 GHRPLDK 48

RESULT 21
US-08-206-176-4
; Sequence 4, Application US/08206176
; Patent No. 5639940
; GENERAL INFORMATION:
; APPLICANT: Garner, Ian
; APPLICANT: Dalrymple, Michael A
; APPLICANT: Prunkard, Donna E
; APPLICANT: Foster, Donald C
; TITLE OF INVENTION: Production of Fibrinogen in Transgenic
; TITLE OF INVENTION: Animals
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,176
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-648
; REFERENCE/DOCKET NUMBER: 93-15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-206-176-4

Query Match      82.0%; Score 41; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 22
US-09-949-016-9617
; Sequence 9617, Application US/09949016
; Patent No. 6812339
```



```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9617
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9617

Query Match      82.0%; Score 41; DB 4; Length 493;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GHRPLDK 7
Db      47 GHRPLDK 53

RESULT 23
US-09-252-991A-18909
; Sequence 18909, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18909
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18909

Query Match      80.0%; Score 40; DB 4; Length 360;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 HRPDLKC 8
Db      184 HRPDLQC 190

RESULT 24
US-09-252-991A-18782
; Sequence 18782, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18782
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18782

Query Match      74.0%; Score 37; DB 4; Length 177;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GHRPLDKC 8
Db      17 GHRPIARC 24

RESULT 25
US-10-142-935-9
; Sequence 9, Application US/10142935
; Patent No. 6835378
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATI
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-9

Query Match      72.0%; Score 36; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GHRPLD 6
Db      5 GHRPLD 10

RESULT 26
US-10-142-935-8
; Sequence 8, Application US/10142935
; Patent No. 6835378
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATI
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-8

Query Match      72.0%; Score 36; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GHRPLD 6
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Db 10 GHRPLD 15

RESULT 27
US-10-142-935-5
; Sequence 5, Application US/10142935
; Patent No. 6835378
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-5

Query Match 72.0%; Score 36; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
| | | | |
Db 15 GHRPLD 20

RESULT 28
US-09-248-796A-26425
; Sequence 26425, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26425
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26425

Query Match 72.0%; Score 36; DB 4; Length 74;
Best Local Similarity 85.7%; Pred. No. 8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 68 GHRPADK 74

RESULT 29
US-09-252-991A-23750
; Sequence 23750, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23750
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23750

Query Match 72.0%; Score 36; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
| | | | |
Db 134 GHRPLD 139

RESULT 30
US-09-252-991A-21990
; Sequence 21990, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21990
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21990

Query Match 71.0%; Score 35.5; DB 4; Length 246;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 GHRPL-DKC 8
| | | | |
Db 124 GHRPLADQC 132

RESULT 31
US-09-270-767-39157
; Sequence 39157, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39157
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-39157

Query Match 70.0%; Score 35; DB 4; Length 155;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
|||:|
Db 6 HRPIDLC 12

RESULT 32

US-09-270-767-54374
; Sequence 54374, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54374
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-54374

Query Match 70.0%; Score 35; DB 4; Length 155;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
|||:|
Db 6 HRPIDLC 12

RESULT 33

US-09-799-875-5
; Sequence 5, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-875-5

Query Match 70.0%; Score 35; DB 4; Length 1203;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 799 GHRPLSK 805

RESULT 34

US-09-258-754-234
; Sequence 234, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 234
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-234

Query Match 68.0%; Score 34; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RPLDKC 8
|||:|
Db 4 RPIDKC 9

RESULT 35

US-09-042-107-234
; Sequence 234, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 234
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-234

Query Match 68.0%; Score 34; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RPLDKC 8
|||:|
Db 4 RPIDKC 9

RESULT 36

US-09-722-250D-234
; Sequence 234, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki

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; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 234
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-234

Query Match          68.0%; Score 34; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 RPLDKC 8
DB      4 RPIDKC 9

RESULT 37
US-09-676-475A-234
; Sequence 234, Application US/09676475A
; Patent No. 6784153
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LA 4377
; CURRENT APPLICATION NUMBER: US/09/676,475A
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 234
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-676-475A-234

Query Match          68.0%; Score 34; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 RPLDKC 8
DB      4 RPIDKC 9

RESULT 38
US-09-248-796A-16727
; Sequence 16727, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
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; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16727
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16727

Query Match          68.0%; Score 34; DB 4; Length 190;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 HRPLDKC 8
DB      109 HRPIDIC 115

RESULT 39
US-08-469-260A-38
; Sequence 38, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-260A-38

Query Match          68.0%; Score 34; DB 4; Length 245;
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Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
Db 25 GRRPLAKC 32

RESULT 40

US-08-488-446-38
; Sequence 38, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/488,446
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-446-38

Query Match 68.0%; Score 34; DB 4; Length 245;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
Db 25 GRRPLAKC 32

Search completed: June 1, 2005, 11:53:57
Job time : 33 secs

Handwritten text, possibly a signature or date, oriented vertically.

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OM protein - protein search, using sw model

Run on: June 1, 2005, 11:44:05 ; Search time 99.7333 Seconds
(without alignments)
27.728 Million cell updates/sec

Title: US-09-424-940A-2

Perfect score: 50

Sequence: 1 GHRPLDK 8

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Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	41	82.0	14	16	US-10-450-073-6
2	41	82.0	20	14	US-10-142-935-6
3	41	82.0	25	14	US-10-142-935-4
4	41	82.0	28	16	US-10-459-030B-294
5	41	82.0	30	14	US-10-131-543-5
6	41	82.0	30	14	US-10-131-546-5
7	41	82.0	30	14	US-10-131-346-5
8	41	82.0	30	15	US-10-415-024-5
9	41	82.0	87	15	US-10-276-774-1709
10	41	82.0	488	10	US-09-919-039-33
11	41	82.0	491	14	US-10-017-724-6
12	39	78.0	67	11	US-09-864-408A-7552
13	38	76.0	136	16	US-10-437-963-114771

14	38	76.0	248	15	US-10-425-114-42547	Sequence 42547, A
15	38	76.0	308	15	US-10-346-198-29	Sequence 29, Appl
16	38	76.0	352	16	US-10-437-963-187345	Sequence 187345,
17	38	76.0	493	16	US-10-437-963-128550	Sequence 128550,
18	38	76.0	548	15	US-10-346-198-78	Sequence 78, Appl
19	38	76.0	626	16	US-10-437-963-187347	Sequence 187347,
20	37	74.0	136	16	US-10-437-963-187113	Sequence 187113,
21	37	74.0	257	16	US-10-437-963-172840	Sequence 172840,
22	37	74.0	482	15	US-10-369-493-6831	Sequence 6831, Ap
23	36	72.0	10	14	US-10-142-935-9	Sequence 9, Appl
24	36	72.0	15	14	US-10-142-935-8	Sequence 8, Appl
25	36	72.0	16	15	US-10-378-674-7	Sequence 7, Appl
26	36	72.0	20	14	US-10-142-935-5	Sequence 5, Appl
27	36	72.0	90	16	US-10-437-963-132166	Sequence 132166,
28	36	72.0	105	11	US-09-864-408A-382	Sequence 382, App
29	36	72.0	479	16	US-10-437-963-127165	Sequence 127165,
30	36	72.0	732	14	US-10-156-761-12627	Sequence 12627, A
31	36	72.0	735	16	US-10-437-963-182675	Sequence 182675,
32	36	72.0	800	16	US-10-437-963-114710	Sequence 114710,
33	35	70.0	74	15	US-10-424-599-175814	Sequence 175814,
34	35	70.0	111	16	US-10-437-963-148809	Sequence 148809,
35	35	70.0	131	16	US-10-437-963-129796	Sequence 129796,
36	35	70.0	240	14	US-10-017-161-1358	Sequence 1358, Ap
37	35	70.0	275	15	US-10-425-114-68291	Sequence 68291, A
38	35	70.0	305	14	US-10-017-161-450	Sequence 450, App
39	35	70.0	305	14	US-10-017-161-468	Sequence 468, App
40	35	70.0	305	14	US-10-025-806-104	Sequence 104, App
41	35	70.0	305	15	US-10-292-798-404	Sequence 404, App
42	35	70.0	305	15	US-10-292-798-418	Sequence 418, App
43	35	70.0	305	15	US-10-041-615-2	Sequence 2, Appl
44	35	70.0	420	15	US-10-424-599-259761	Sequence 259761,
45	35	70.0	1052	15	US-10-236-417-156	Sequence 156, App

ALIGNMENTS

RESULT 1
US-10-450-073-6
; Sequence 6, Application US/10450073
; Publication No. US20040132969A1
; GENERAL INFORMATION:
; APPLICANT: Melvin, William T
; APPLICANT: Thompson, William D
; APPLICANT: Stirk, Christina M
; TITLE OF INVENTION: Antibodies, Peptides, Analogs and Uses Thereof
; FILE REFERENCE: 0380-P0321300
; CURRENT APPLICATION NUMBER: US/10/450,073
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/05505
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: GB 0030309.9
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesised
US-10-450-073-6

Query Match 82.0%; Score 41; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7

Db 1 GHRPLDK 7

RESULT 2

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US-10-142-935-6
; Sequence 6, Application US/10142935
; Publication No. US20030044418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-6

Query Match      82.0%; Score 41; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GHRPLDK 7
Db      10 GHRPLDK 16

RESULT 3
US-10-142-935-4
; Sequence 4, Application US/10142935
; Publication No. US20030044418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-4

Query Match      82.0%; Score 41; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GHRPLDK 7
Db      15 GHRPLDK 21

RESULT 4
US-10-459-030B-294
; Sequence 294, Application US/10459030B
; Publication No. US20040192596A1
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12

US-10-142-935-5
; Sequence 5, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-543-5

Query Match      82.0%; Score 41; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GHRPLDK 7
Db      4 GHRPLDK 10

RESULT 6
US-10-131-546-5
; Sequence 5, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
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; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-546-5

Query Match 82.0%; Score 41; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 4 GHRPLDK 10

RESULT 7

US-10-131-346-5
; Sequence 5, Application US/10131346
; Publication No. US20030103899A1
; GENERAL INFORMATION:

; APPLICANT: CyZ, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC 6-HYDROXY CHROMANS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-346-5

Query Match 82.0%; Score 41; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 4 GHRPLDK 10

RESULT 8

US-10-415-024-5
; Sequence 5, Application US/10415024
; Publication No. US20040058984A1
; GENERAL INFORMATION:

; APPLICANT: Diatide, Inc.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; TITLE OF INVENTION: CHROMANS
; FILE REFERENCE: 09744-015W01
; CURRENT APPLICATION NUMBER: US/10/415,024
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992

; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-415-024-5

Query Match 82.0%; Score 41; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 4 GHRPLDK 10

RESULT 9

US-10-276-774-1709
; Sequence 1709, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1709
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)...(87)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-276-774-1709

Query Match 82.0%; Score 41; DB 15; Length 87;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 31 GHRPLDK 37

RESULT 10

US-09-919-039-33
; Sequence 33, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaeer, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 3393861CD1
US-09-919-039-33

Query Match 82.0%; Score 41; DB 10; Length 488;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 42 GHRPLDK 48

RESULT 11
US-10-017-724-6
; Sequence 6, Application US/10017724
; Publication No. US2003009958A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: WMI-004
; CURRENT APPLICATION NUMBER: US/10/017,724
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/329,958
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-017-724-6

Query Match 82.0%; Score 41; DB 14; Length 491;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 12
US-09-864-408A-7552
; Sequence 7552, Application US/09864408A
; Publication No. US2004000947A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: No. US2004000947A1 Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7552
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-7552

Query Match 78.0%; Score 39; DB 11; Length 67;
Best Local Similarity 75.0%; Pred. No. 8.8;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 8
Db 57 GHRPLDK 64

RESULT 13
US-10-437-963-114771
; Sequence 114771, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 114771
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(136)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_1842C.1.pep
US-10-437-963-114771

Query Match 76.0%; Score 38; DB 16; Length 136;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDK 8
Db 117 GHRPLSAC 124

RESULT 14
US-10-425-114-42547
; Sequence 42547, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 42547
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700224123_FLI.pep

US-10-425-114-42547

Query Match 76.0%; Score 38; DB 15; Length 248;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
|||||:|
DB 29 GHRPLCRC 36

RESULT 15

US-10-346-198-29
; Sequence 29, Application US/10346198
; Publication No. US20040043485A1
; GENERAL INFORMATION:
; APPLICANT: WESSLER, SUSAN R.
; APPLICANT: JIANG, NING
; APPLICANT: BAO, ZHIRONG
; APPLICANT: ZHANG, XIAOYU
; APPLICANT: EDDY, SEAN R.
; TITLE OF INVENTION: TRANSPOSABLE ELEMENTS IN RICE AND METHODS OF USE
; FILE REFERENCE: 18465-0018
; CURRENT APPLICATION NUMBER: US/10/346,198
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 60/337,409
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-346-198-29

Query Match 76.0%; Score 38; DB 15; Length 308;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
|||||
DB 120 GHSPLQKC 127

RESULT 16

US-10-437-963-187345
; Sequence 187345, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 187345
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_84057C.1.pep
US-10-437-963-187345

Query Match 76.0%; Score 38; DB 16; Length 352;
Best Local Similarity 75.0%; Pred. No. 68;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GHRPLDKC 8
|||||
DB 119 GHSPLQKC 126

RESULT 17

US-10-437-963-128550
; Sequence 128550, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128550
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(493)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30894C.1.pep
US-10-437-963-128550

Query Match 76.0%; Score 38; DB 16; Length 493;
Best Local Similarity 75.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
|||||
DB 120 GHSPLQKC 127

RESULT 18

US-10-346-198-78
; Sequence 78, Application US/10346198
; Publication No. US20040043485A1
; GENERAL INFORMATION:
; APPLICANT: WESSLER, SUSAN R.
; APPLICANT: JIANG, NING
; APPLICANT: BAO, ZHIRONG
; APPLICANT: ZHANG, XIAOYU
; APPLICANT: EDDY, SEAN R.
; TITLE OF INVENTION: TRANSPOSABLE ELEMENTS IN RICE AND METHODS OF USE
; FILE REFERENCE: 18465-0018
; CURRENT APPLICATION NUMBER: US/10/346,198
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 60/337,409
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-346-198-78

Query Match 76.0%; Score 38; DB 15; Length 548;
Best Local Similarity 75.0%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
| | | | |
Db 229 GHSPLQKC 236

RESULT 19

US-10-437-963-187347
; Sequence 187347, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 187347
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_84059C.1.pep
US-10-437-963-187347

Query Match 76.0%; Score 38; DB 16; Length 626;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
| | | | |
Db 307 GHSPLQKC 314

RESULT 20

US-10-437-963-187113
; Sequence 187113, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 187113
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_83849C.1.pep
US-10-437-963-187113

Query Match 74.0%; Score 37; DB 16; Length 136;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
| | | | |
Db 67 GRRPLDSC 74

RESULT 21

US-10-437-963-172840
; Sequence 172840, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172840
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70938C.1.pep
US-10-437-963-172840

Query Match 74.0%; Score 37; DB 16; Length 257;
Best Local Similarity 75.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
| | | | |
Db 94 GRRPLDSC 101

RESULT 22

US-10-369-493-6831
; Sequence 6831, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6831
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6831

Query Match 74.0%; Score 37; DB 15; Length 482;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
| | | | |
Db 155 HRPLDVC 161

```
RESULT 23
US-10-142-935-9
; Sequence 9, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-9
Query Match 72.0%; Score 36; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
   |||||
Db 5 GHRPLD 10

RESULT 24
US-10-142-935-8
; Sequence 8, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-8
Query Match 72.0%; Score 36; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
   |||||
Db 10 GHRPLD 15

RESULT 25
US-10-378-674-7
; Sequence 7, Application US/10378674
; Publication No. US20040006209A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATIVE
; TITLE OF INVENTION: STAPHYLOCOCCAL PROTEINS
; FILE REFERENCE: P07556US01/BAS
; CURRENT APPLICATION NUMBER: US/10/378,674
; CURRENT FILING DATE: 2003-03-05
```

```
; PRIOR APPLICATION NUMBER: 60/361,324
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-378-674-7
Query Match 72.0%; Score 36; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
   |||||
Db 11 GHRPLD 16

RESULT 26
US-10-142-935-5
; Sequence 5, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-5
Query Match 72.0%; Score 36; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
   |||||
Db 15 GHRPLD 20

RESULT 27
US-10-437-963-132166
; Sequence 132166, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 132166
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_34161C.1.pep
US-10-437-963-132166

Query Match 72.0%; Score 36; DB 16; Length 90;
Best Local Similarity 71.4%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HRPLDKC 8
Db 37 HRPIDAC 43

RESULT 28

US-09-864-408A-382
; Sequence 382, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encoded
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/286,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-382

Query Match 72.0%; Score 36; DB 11; Length 105;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RPLDKC 8
Db 60 RPLDKC 65

RESULT 29

US-10-437-963-127165
; Sequence 127165, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 127165
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_29643C.1.pep
US-10-437-963-127165

Query Match 72.0%; Score 36; DB 16; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLD 6
Db 32 GHRPLD 37

RESULT 30

US-10-156-761-12627
; Sequence 12627, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12627
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12627

Query Match 72.0%; Score 36; DB 14; Length 732;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLD 6
Db 344 GHRPLD 349

RESULT 31

US-10-437-963-182675
; Sequence 182675, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 182675
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79840C.1.pep
US-10-437-963-182675

Query Match 72.0%; Score 36; DB 16; Length 735;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLD 6

Db 94 GHRPLD 99
|||||

RESULT 32

US-10-437-963-114710
; Sequence 114710, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 114710
; LENGTH: 800

; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_18374C.1.pep
US-10-437-963-114710

Query Match 72.0%; Score 36; DB 16; Length 800;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
|||||

Db 243 HRPLESC 249

RESULT 33

US-10-424-599-175814
; Sequence 175814, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 175814
; LENGTH: 74

; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

; NAME/KEY: unsure
; LOCATION: (1)..(74)

; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_129779C.1.pep
US-10-424-599-175814

Query Match 70.0%; Score 35; DB 15; Length 74;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
|||||

Db 41 HRPLDK 46

RESULT 34

US-10-437-963-148809
; Sequence 148809, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 148809
; LENGTH: 111
; TYPE: PRT

; ORGANISM: Oryza sativa
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_49202C.1.pep
US-10-437-963-148809

Query Match 70.0%; Score 35; DB 16; Length 111;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
|||||

Db 94 HRPLQRC 100

RESULT 35

US-10-437-963-129796
; Sequence 129796, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 129796
; LENGTH: 131

; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_32018C.1.pep
US-10-437-963-129796

Query Match 70.0%; Score 35; DB 16; Length 131;
Best Local Similarity 75.0%; Pred. No. 96;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
|||||

Db 94 GHRPLGCC 101

RESULT 36

US-10-017-161-1358
; Sequence 1358, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1358
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(41)
; OTHER INFORMATION: Variable amino acid
US-10-017-161-1358

Query Match 70.0%; Score 35; DB 14; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
Db 155 HRPLDK 160
|||||

RESULT 37

US-10-425-114-68291
; Sequence 68291, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68291
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO1726GH05_FLI.pep
US-10-425-114-68291

Query Match 70.0%; Score 35; DB 15; Length 275;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDK 8
Db 126 GHRPLVK 133
|||||

RESULT 38

US-10-017-161-450
; Sequence 450, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 450
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-450

Query Match 70.0%; Score 35; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
Db 220 HRPLDK 225
|||||

RESULT 39

US-10-017-161-468
; Sequence 468, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 468
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-468

Query Match 70.0%; Score 35; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
Db 220 HRPLDK 225
|||||

RESULT 40

US-10-025-806-104
; Sequence 104, Application US/10025806
; Publication No. US20030198955A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Ballinger, Robert
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Colman, Steven


```

; APPLICANT: Spytek, Kimberly
; APPLICANT: Caaman, Stacie
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Sciore, Paul
; APPLICANT: Smithson, Glenda
; APPLICANT: Peyman, John
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Vernet, Corine
; APPLICANT: Shenoy, Suresh
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Tchernev, Velizar
; APPLICANT: Anderson, David
; APPLICANT: Gusev, Vladimir
; APPLICANT: Malyankar, Uriel
; APPLICANT: Zhong, Haihong
; APPLICANT: Ellerman, Karen
; APPLICANT: Wolenc, Adam
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-224 AB
; CURRENT APPLICATION NUMBER: US/10/025,806
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,635
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/259,743
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/299,327
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 60/261,498
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/263,689
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/276,464
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/271,021
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/275,946
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/278,150
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/285,718
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 60/312,902
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/257,876
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/260,718
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/284,591
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-806-104

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Query Match      70.0%; Score 35; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 HRPDK 7
      |||||
Db      220 HRPDK 225

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Search completed: June 1, 2005, 11:57:10
Job time : 100.733 secs

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OM protein - protein search, using sw model

Run on: June 1, 2005, 11:41:15 ; Search time 25.6 Seconds
(without alignments)
30.068 Million cell updates/sec

Title: US-09-424-940A-2

Perfect score: 50

Sequence: 1 GHRPLDKC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	41	82.0	31	2 A05297	fibrinogen beta ch
2	41	82.0	491	1 FGHUB	fibrinogen beta ch
3	39	78.0	725	2 A86328	protein F18014.27
4	37	74.0	82	2 D82773	hypothetical prote
5	37	74.0	482	2 T15829	hypothetical prote
6	37	74.0	518	2 B84514	probable cytochrom
7	37	74.0	591	2 S73790	hypothetical prote
8	36	72.0	201	2 C95399	probable transcrip
9	36	72.0	240	2 AE2632	hypothetical prote
10	36	72.0	468	1 FGBOB	fibrinogen beta'ch
11	36	72.0	1490	2 T47840	multi resistance p
12	35	70.0	463	2 A38463	fibrinogen beta ch
13	35	70.0	562	2 T27807	hypothetical prote
14	35	70.0	615	2 D96499	probable UDP-gluc
15	35	70.0	1071	2 T18307	suppressor protein
16	34	68.0	122	1 WILAI	alpha-amylase/try
17	34	68.0	130	1 TNLJGG	trans-activating t
18	34	68.0	130	2 S12157	trans-activating t
19	34	68.0	409	2 F90825	probable integrase
20	34	68.0	416	2 A85684	hypothetical prote
21	34	68.0	421	2 T29789	hypothetical prote
22	34	68.0	673	2 T40817	zinc finger protei
23	34	68.0	782	2 JC7284	phospholipase A2 (
24	34	68.0	795	2 A84608	hypothetical prote
25	34	68.0	911	2 T29134	hypothetical prote
26	34	68.0	1576	2 T03277	pol protein - yeas
27	33	66.0	225	2 A75550	MutT/nudix family
28	33	66.0	325	2 H95278	conserved hypotet
29	33	66.0	326	2 AD2936	polymerase epsilon

30	33	66.0	326	2 C98346	hypothetical prote
31	33	66.0	353	2 T52184	zinc transporter Z
32	33	66.0	427	2 AB3025	methionine gamma-L
33	33	66.0	427	2 G98259	methionine gamma-L
34	33	66.0	485	2 A70706	probable phoR prot
35	33	66.0	1058	2 D82654	ankyrin-like prote
36	33	66.0	1635	2 T14075	chitinase (EC 3.2.
37	32	64.0	73	2 S46349	trans-activating t
38	32	64.0	116	2 T17674	hypothetical prote
39	32	64.0	189	2 E82256	conserved hypotet
40	32	64.0	296	2 B71305	hypothetical prote
41	32	64.0	309	2 S40749	hypothetical prote
42	32	64.0	372	2 H81291	hypothetical prote
43	32	64.0	374	2 F97257	glycosyltransferas
44	32	64.0	383	2 T23182	hypothetical prote
45	32	64.0	423	2 T20233	hypothetical prote

ALIGNMENTS

RESULT 1

A05297
fibrinogen beta chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 05-Jun-1987 #sequence revision 05-Jun-1987 #text change 09-Jul-2004
C:Accession: B94308; A03123; A37512; A05297; B37512; D03118
R:Birken, S.; Wilner, G.D.; Canfield, R.E.
Thromb. Res. 7, 599-610, 1975
A:Title: Studies of the structure of canine fibrinogen.
A:Reference number: A94308; MUID:76081726; PMID:1198547
A:Accession: B94308
A:Molecule type: protein
A:Residues: 1-31 <BIR>
A:Cross-references: UNIPROT:P02677
R:Blomback, B.; Blomback, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A:Title: Studies on fibrinopeptides from mammals.
A:Reference number: A03118
A:Accession: A03123
A:Molecule type: protein
A:Residues: 1-19 <BLQ>
R:Krajewski, T.; Blomback, B.
Acta Chem. Scand. 22, 1339-1346, 1968
A:Reference number: A37512; MUID:69066367; PMID:5727635
A:Accession: A37512
A:Molecule type: protein
A:Residues: 1-19 <KRA>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf.
C:Keywords: blood coagulation; liver; plasma; sulfoprotein
F:1-19/Product: fibrinopeptide B #status experimental <APR>
F:2/Binding site: sulfate (Tyr) (covalent) #status experimental
F:3/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 82.0% Score 41; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

Db 20 GHRPLDK 26

RESULT 2

FGHUB
fibrinogen beta chain precursor [validated] - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide B
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence revision 31-Mar-1993 #text change 09-Jul-2004
C:Accession: B43568; A90469; B90469; I37389; A94433; A90437; A94309; G54223; A03121; B37
R:Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990

Annu. Rev. Biochem. 53, 195-229, 1984

A>Title: Fibrinogen and fibrin.

A|Reference number: A90041; MUID:84305751; PMID:6383194

A|Contents: annotation; review, EM structure, Polymerization, ligands

R|Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.

Ann. N. Y. Acad. Sci. 408, 449-456, 1983

A>Title: Cloning of fibrinogen genes and their cDNA.

A|Reference number: A90038; MUID:83254384; PMID:6575700

A|Contents: annotation

R|Kirschbaum, N.E.; Budzynski, A.Z.

J. Biol. Chem. 265, 13669-13676, 1990

A>Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-term

A|Reference number: A37117; MUID:90337977; PMID:2143188

A|Contents: annotation; hementin cleavage site

A|Note: hementin, a protease from Haemeteria ghiliani, the giant South American leech,

C|Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves

C|Comment: The soft clot is converted into the hard clot.

C|Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliz

C|Comment: All fibrinogen chains are synthesized in the liver.

C|Genetics:

A|Gene: GDB:FGB

A|Cross-references: GDB:119130; OMIM:134830

A|Map position: 4q28-4q28

A|Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2

C|Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FGF

ins are contained in the core. Two three-chain coiled coils emerge from this core and cor

from the distal domain nodes.

C|Function:

A|Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into f

A|Pathway: blood coagulation

C|Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfidic

C|Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglytamic ac

F|1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>

F|31-43/Product: fibrinogen beta chain #status experimental <MAT>

F|31-44/Product: fibrinopeptide B #status experimental <APT>

F|45-49/Product: fibrin beta chain #status experimental <FGB>

F|45-47/Region: polymerization site

F|99-228/Domain: fibrinogen disulfide ring homology <FDR>

F|238-487/Domain: fibrinogen beta/gamma homology <FBG>

F|31/Modified site: Pyrrrolidone carboxylic acid (Gln) (in mature form) #status experiment

F|44-45/Cleavage site: Arg-Gly (thrombin) #status experimental

F|95/Disulfide bonds: interchain (to alpha-55) #status experimental

F|106/Disulfide bonds: interchain (to alpha-68) #status experimental

F|110/Disulfide bonds: interchain (to gamma-45) #status experimental

F|223/Disulfide bonds: interchain (to alpha-184) #status experimental

F|227/Disulfide bonds: interchain (to gamma-161) #status experimental

F|231-316,241-270,424-437/Disulfide bonds: #status experimental

F|394/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 82.0%; Score 41; DB 1; Length 491;
Best Local Similarity 100.0%; Pred.No.3,2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
||||||
Db 45 GHRPLDK 51

RESULT 3

A86328

protein F18014.27 [imported] - Arabidopsis thaliana

C|Species: Arabidopsis thaliana (mouse-ear cress)

C|Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C|Accession: A86328

R|Theologian, A.; Ecker, J.R.; Palm, C.J.; Federgpiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A|Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzalli,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A|Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: A86328
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-725 <STO>
 A;Cross-references: UNIPROT:Q9LN43; GB:AE005172; NID:g8778424; PIDN:AAF79432.1; GSPDB:GN
 C;Genetics:
 A;Gene: F18014.27
 A;Map position: 1

Query Match 78.0%; Score 39; DB 2; Length 725;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
 |||||
 Db 555 GHKPDCKC 562

RESULT 4
 D82773
 hypothetical protein XF0702 [imported] - *Xylella fastidiosa* (strain 9a5c)
 C;Species: *Xylella fastidiosa*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: D82773
 R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below
 A;Accession: D82773
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-82 <STO>
 A;Cross-references: UNIPROT:Q9PFF7; GB:AE003913; GB:AE003849; NID:g9105578; PIDN:AAF8351
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Mencia, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.C.R.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A;Reference number: A59328
 A;Contents: annotation
 C;Genetics:
 A;Gene: XF0702

Query Match 74.0%; Score 37; DB 2; Length 82;
 Best Local Similarity 75.0%; Pred. No. 3.5;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
 |||||
 Db 59 GHSPGLKC 66

RESULT 5
 T15829
 hypothetical protein C53C9.3 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T15829
 R;Bentley, D.
 submitted to the EMBL Data Library, June 1995
 A;Description: The sequence of *C. elegans* cosmid C53C9.

A;Reference number: Z18413

A;Accession: T15829

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-482 <BEN>

A;Cross-references: UNIPROT:Q09937; EMBL:U28734; NID:g861255; PID:g1945480; PIDN:AAB5260

A;Experimental source: strain Bristol N2; clone C53C9

C;Genetics:

A;Gene: CESP:C53C9.3

A;Map position: X

A;Introns: 19/2; 49/3; 128/3; 189/2; 203/3; 254/3; 273/1; 311/2; 372/2; 449/1

Query Match 74.0%; Score 37; DB 2; Length 482;
 Best Local Similarity 85.7%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HRPLDKC 8
 |||||
 Db 155 HRPLDVC 161

RESULT 6

B84514

probable cytochrome P450 [imported] - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: B84514

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: B84514

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-518 <STO>

A;Cross-references: UNIPROT:Q9S149; GB:AE002093; NID:g4587680; PIDN:AAD25850.1; GSPDB:GN

C;Genetics:

A;Map position: 2

A;Gene: At2g14100

C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C;Keywords: heme; iron; metalloprotein

F;453/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 74.0%; Score 37; DB 2; Length 518;
 Best Local Similarity 62.5%; Pred. No. 21;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
 |||||
 Db 112 GHPPIDEC 119

RESULT 7

S73790

hypothetical protein A19_ORF591 - *Mycoplasma pneumoniae* (strain ATCC 29342)

C;Species: *Mycoplasma pneumoniae*

A;Variety: ATCC 29342

C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S73790

R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A;Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae*

A;Reference number: S73327; MUID:97105885; PMID:8948633

A;Accession: S73790

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-591 <HIM>

A;Cross-references: UNIPROT:P75409; EMBL:AE000046; GB:U00089; NID:g1674152; PIDN:AAB9611

C;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C;Genetics:

A;Genetic code: SGC3

C;Superfamily: Mycoplasma pneumoniae hypothetical protein A19_ORF591

Query Match 74.0%; Score 37; DB 2; Length 591;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
| | | | |
Db 240 GENPLDKC 247

RESULT 8

C95399
probable transcription regulator [imported] - Sinorhizobium meliloti (strain 1021) magae
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95399
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95399
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-201 <KUR>
A;Cross-references: UNIPROT:Q92XY9; GB:AE006469; PIDN:AAK65757.1; PID:g14524255; GSPDB:C
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMA2008
A;Genome: plasmid

Query Match 72.0%; Score 36; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
| | | | |
Db 175 GHRPLD 180

RESULT 9

AE2632
hypothetical protein Atu0456 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AE2632
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE2632
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-240 <KUR>
A;Cross-references: UNIPROT:Q8U144; GB:AE008688; PIDN:AAL41475.1; PID:g17738801; GSPDB:C
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0456
A;Map position: circular chromosome

Query Match 72.0%; Score 36; DB 2; Length 240;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
| | | | |
Db 144 HRPLDKC 150

RESULT 10

PG80B
fibrinogen beta chain - bovine
N;Contains: fibrinopeptide B
C;Species: Bos primigenius taurus (cattle)
C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 13-Sep-1996
C;Accession: A03122; B03117; B37507; A37513; S02443
R;Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A;Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
A;Reference number: A03122
A;Accession: A03122
A;Molecule type: protein
A;Residues: 1-4 <BLO>
R;Sjoquist, J.; Blomback, B.; Wallen, P.
Ark. Kemi 16, 425-436, 1960
A;Title: Amino acid sequence of bovine fibrinopeptides.
A;Reference number: A03117
A;Accession: B03117
A;Molecule type: protein
A;Residues: 5-21 <SUO>
R;Martinielli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S
Arch. Biochem. Biophys. 192, 27-32, 1979
A;Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrinogen
A;Reference number: A37507; MUID:79164394; PMID:434821
A;Accession: B37507
A;Molecule type: protein
A;Residues: 22-53 <WAR>
R;Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
A;Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
A;Reference number: A37513; MUID:81199473; PMID:6262803
A;Accession: A37513
A;Molecule type: mRNA
A;Residues: 44-468 <CHU>
R;Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
FEBS Lett. 232, 56-60, 1988
A;Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
A;Reference number: S02443; MUID:88211875; PMID:2966748
A;Accession: S02443
A;Molecule type: protein
A;Residues: 373-374 <MED>
C;Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
C;Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alpha
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
F;76-205/Domain: fibrinogen disulfide ring homology <FDR>
F;215-464/Domain: fibrinogen beta/gamma homology <FBG>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;5/Binding site: sulfate (Tyr) (covalent) #status experimental
F;21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
F;371/Binding site: carboxylate (Asn) (covalent) #status predicted
F;372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match 72.0%; Score 36; DB 1; Length 468;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 22 GHRPYDK 28

RESULT 11

T47840
multi resistance protein homolog - Arabidopsis thaliana
N;Alternate names: protein T209.140
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47840
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24475
A;Accession: T47840
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1490 <NYA>
A;Cross-references: UNIPROT:Q9M1C7; EMBL:AL138658
A;Experimental source: cultivar Columbia, BAC clone T209
C;Genetics:
A;Map position: 3
A;Intons: 9/1; 795/3; 824/3; 1036/3; 1075/3; 1174/1; 1245/3; 1347/3; 1369/1; 1449/1
A;Note: T209.140
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 72.0%; Score 36; DB 2; Length 1490;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6

|||||

DB 1226 GHRPLD 1231

RESULT 12

A38463
fibrinogen beta chain - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
C;Accession: A38463
R;Weisbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
Biochemistry 30, 3290-3294, 1991
A;Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage site
A;Reference number: A38463; MUID:91182745; PMID:2009266
A;Accession: A38463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-463 <WEI>
A;Cross-references: UNIPROT:Q02020; GB:W58514; NID:g211779; PIDN:AAA48770.1; PID:g211780
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
F;73-202/Domain: fibrinogen disulfide ring homology <FDR>
F;212-460/Domain: fibrinogen beta/gamma homology <PBG>

Query Match 70.0%; Score 35; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7

|||||

DB 19 HRPLDK 24

RESULT 13

T27807
hypothetical protein ZK265.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27807
R;Dobson, R.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z20422
A;Accession: T27807
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-562 <WLL>
A;Cross-references: UNIPROT:Q94400; EMBL:Z81143; PIDN:CA803514.1; GSPDB:GN00019; CESP:ZK

A;Experimental source: clone ZK265

C;Genetics:

A;Gene: CESP:ZK265.1

A;Map position: 1

A;Intons: 19/2; 46/3; 93/2; 219/2; 274/3; 319/2; 362/3; 431/3; 482/1

Query Match 70.0%; Score 35; DB 2; Length 562;
Best Local Similarity 62.5%; Pred. No. 55;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8

|||||

DB 404 GYRPIDYC 411

RESULT 14

D96499

probable UDP-glucose,sterol glucosyltransferase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D96499
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D96499
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-615 <STO>
A;Cross-references: UNIPROT:Q9XIG1; GB:AE005173; NID:g5080759; PIDN:AAD39269.1; GSPDB:GN

Query Match 70.0%; Score 35; DB 2; Length 615;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8

|||||

DB 48 GHRGLDHC 55

RESULT 15

T18307

suppressor protein - yeast (Kluyveromyces marxianus var. lactis)
C;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C;Accession: T18307
R;Groom, K.R.; Heyman, H.C.; Steffen, M.C.; Hawkins, L.; Martin, N.C.
Yeast 14, 77-87, 1998
A;Title: Kluyveromyces lactis SEF1 and its Saccharomyces cerevisiae homologue bypass the
A;Reference number: Z13599; MUID:98144791; PMID:9483797
A;Accession: T18307
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1071 <GRO>
A;Cross-references: UNIPROT:P87164; EMBL:U92898; NID:g2104692; PID:g2104693; PIDN:AAC3939

A;Gene: SEF1

C;Superfamily: GAL4 zinc binuclear cluster homology

F;81-121/Domain: GAL4 zinc binuclear cluster homology <GL4>

Query Match 70.0%; Score 35; DB 2; Length 1071;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY      1 GHRPLDKC 8
      ||||: |
Db      79 GHRPVTSC 86

RESULT 16
WILLAI
alpha-amylase/trypsin inhibitor - finger millet
C;Species: Eleusine coracana (finger millet)
C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01326
R;Campose, F.A.P.; Richardson, M.
FEBS Lett. 152, 300-304, 1983
A;Title: The complete amino acid sequence of the bifunctional alpha-amylase/trypsin inhibitor
A;Reference number: A01326
A;Accession: A01326
A;Molecule type: protein
A;Residues: 1-122 <CW>
A;Cross-references: UNIPROT:P01087
A;Note: 25-Ser, 28-Thr, and 70-Ser were also found
C;Superfamily: wheat alpha-amylase inhibitor
C;Keywords: alpha-amylase inhibitor; serine proteinase inhibitor
F;34/Inhibitory site: ARG (trypsin) #status Predicted

      Query Match      68.0%; Score 34; DB 1; Length 122;
      Best Local Similarity 71.4%; Pred. No. 20;
      Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 HRPLDKC 8
      ||||| |
Db      14 HNPLDSC 20

RESULT 17
TNLJGG
trans-activating transcription regulator - human immunodeficiency virus type 2 (isolate
N;Alternate names: tat protein
C;Species: human immunodeficiency virus type 2, HIV-2
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C;Accession: JS0332
R;Hasegawa, A.; Tsujimoto, H.; Maki, N.; Ishikawa, K.; Miura, T.; Fukasawa, M.; Miki, K.
AIDS Res. Hum. Retroviruses 5, 593-604, 1989
A;Title: Sequence of a distinct HIV-2 isolate from Ghana showing significant divergence
A;Reference number: JS0327; MUID:90122350; PMID:2611042
A;Accession: JS0332
A;Molecule type: DNA
A;Residues: 1-130 <HAS>
A;Cross-references: UNIPROT:P18044; GB:M30895; GB:D00477; NID:G325709; PIDN:AAA43929.1;
A;Note: this sequence was submitted to JIPID, October 1989
C;Genetics:
A;Gene: tat
A;Introns: 99/2
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: AIDS; transcription regulation

      Query Match      68.0%; Score 34; DB 1; Length 130;
      Best Local Similarity 71.4%; Pred. No. 21;
      Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 HRPLDKC 8
      ||||| |
Db      44 HRPLEAC 50

RESULT 18
S12157
trans-activating transcription regulator - human immunodeficiency virus type 2
C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S12157
R;Kuehnelt, H.; Kreutz, R.; Ruebsamen-Waigmann, H.

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Nucleic Acids Res. 18, 6142, 1990
A;Title: Nucleotide sequence of HIV-2(D194), an isolate from a Gambian case of 'Neuro-AI
A;Reference number: S12152; MUID:91045094; PMID:2235509
A;Accession: S12157
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-130 <KUE>
A;Cross-references: UNIPROT:P17759; EMBL:X52223; NID:G60155; PIDN:CAA36469.1; PID:G76310
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1990
C;Genetics:
A;Introns: 99/2
C;Superfamily: AIDS trans-activating transcription regulator
C;Keywords: transcription regulation

      Query Match      68.0%; Score 34; DB 2; Length 130;
      Best Local Similarity 71.4%; Pred. No. 21;
      Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 HRPLDKC 8
      ||||| |
Db      44 HRPLEAC 50

RESULT 19
F90825
Probable integrase [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90825
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90825
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-409 <HAY>
A;Cross-references: UNIPROT:Q8X775; GB:BA000007; PIDN:BA834997.1; PID:gl3361038; GSPDB:G
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECs1574
C;Superfamily: phage phi-80 integrase

      Query Match      68.0%; Score 34; DB 2; Length 409;
      Best Local Similarity 75.0%; Pred. No. 64;
      Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GHRPLDKC 8
      ||||| |
Db      144 GAMPLDKC 151

RESULT 20
A85684
Probable integrase of prophage CP-933C Z1835 [imported] - Escherichia coli (strain O157:
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A85684
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Groetbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85684
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-416 <STO>
A;Cross-references: UNIPROT:Q8X775; GB:AE005174; NID:gl2514755; PIDN:AAG55933.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1835
C;Superfamily: phage phi-80 integrase

```


Query Match 68.0%; Score 34; DB 2; Length 416;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
| | | | |
Db 151 GAMPLDKC 158

RESULT 21

T29789
hypothetical protein F44A2.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29789

R;Du, Z.; Le, T.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid F44A2.

A;Reference number: Z20686

A;Accession: T29789

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-421 <DUZ>

A;Cross-references: UNIPROT:Q20381; EMBL:U41993; PIDN:AAA83447.1; CESP:F44A2.2

A;Gene: CESP:F44A2.2

A;Introns: 144/3; 224/2; 278/1; 328/1

Query Match 68.0%; Score 34; DB 2; Length 421;
Best Local Similarity 71.4%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
| | | | |
Db 100 HRPMDIC 106

RESULT 22

T40817
zinc finger protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40817

R;Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, October 1998

A;Reference number: Z21949

A;Accession: T40817

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-673 <BEC>

A;Cross-references: UNIPROT:O94271; EMBL:AL032684; PIDN:CAA21808.1; GSPDB:GN000067; SPDB:

A;Experimental source: strain 972h-; clone p1 p8B7

C;Genetics:

A;Gene: SPDB:SPBP8B7.23

A;Map position: 2

F;210-278/Domain: RING finger homology <RRN>

Query Match 68.0%; Score 34; DB 2; Length 673;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 160 GHRPMDK 166

RESULT 23

JC7284
phospholipase A2 (EC 3.1.1.4) 2, calcium-independent - human
N;Alternate names: membrane-associated calcium-independent phospholipase A2
C;Species: Homo sapiens (man)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C;Accession: JC7284

R;Tanaka, H.; Takeya, R.; Sumimoto, H.

Biochem. Biophys. Res. Commun. 272, 320-326, 2000

A;Title: A novel intracellular membrane-bound calcium-independent phospholipase A2.

A;Reference number: JC7284

A;Accession: JC7284

A;Molecule type: mRNA

A;Residues: 1-782 <TAN>

A;Cross-references: UNIPROT:Q9NP80; DDBJ:AB041261

C;Genetics:

A;Gene: iplA2-2

A;Map position: 7q31

C;Keywords: carboxylic ester hydrolase; membrane-associated protein

Query Match 68.0%; Score 34; DB 2; Length 782;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
| | | | |
Db 496 HMPLDEC 502

RESULT 24

A84608

hypothetical protein At2g22020 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: A84608

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84608

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-795 <STO>

A;Cross-references: UNIPROT:Q9SI27; GB:AE002093; NID:g4417294; PIDN:AAD20419.1; GSPDB:GN

C;Genetics:

A;Gene: At2g22020

A;Map position: 2

Query Match 68.0%; Score 34; DB 2; Length 795;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 41 GHRPLER 47

RESULT 25

T29134

hypothetical protein C09D4.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T29134

R;Wu, X.; Le, T.T.

submitted to the EMBL Data Library, May 1997

A;Description: The sequence of C. elegans cosmid C09D4.

A;Reference number: Z20576

A;Accession: T29134

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-911 <WUX>

A;Cross-references: UNIPROT:O01731; EMBL:AF002196; PIDN:AAB53981.1; GSPDB:GN000019; CESP:

A;Experimental source: strain Bristol N2; clone C09D4

C;Genetics:

A;Gene: CESP:C09D4.4

A;Map position: 1

A;Introns: 277/1; 55/2; 89/1; 117/2; 187/3; 232/1; 284/1; 356/2; 380/3; 430/3; 492/1; 527/

C;Superfamily: Caenorhabditis elegans hypothetical protein C09D4.4

Query Match 68.0%; Score 34; DB 2; Length 911;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RPLDKC 8
|||:|
Db 310 RPIDKC 315

RESULT 26

T03277

pol protein - yeast (Candida albicans) retrotransposon pCal (fragment)

C;Species: Candida albicans

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C;Accession: T03277

R;Matthews, G.D.; Goodwin, T.J.D.; Butler, M.I.; Berryman, T.A.; Poulter, R.T.M.

J. Bacteriol. 179, 7118-7128, 1997

A;Title: pCal, a highly unusual ty1/copia retrotransposon from the pathogenic yeast Candida albicans

A;Reference number: Z14877; MUID:98037512; PMID:9371461

A;Accession: T03277

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1576 <MAT>

A;Cross-references: UNIPROT:O13308; EMBL:AF007776; NID:92636718; PIDN:AAC49878.1; PID:94

C;Genetics:

A;Mobile element: retrotransposon pCal

Query Match 68.0%; Score 34; DB 2; Length 1576;

Best Local Similarity 71.4%; Pred. No. 2.4e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPDLKC 8
|||:|
Db 1506 HRPIDC 1512

RESULT 27

A75550

MutT/nudix family protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: A75550

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: A75550

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-225 <WHI>

A;Cross-references: UNIPROT:Q9RXW3; GB:AE001881; GB:AE000513; NID:96457853; PIDN:AAF0977

A;Experimental source: strain R1

C;Genetics:

A;Gene: DR0192

A;Map position: 1

C;Superfamily: NUDIX hydrolase

Query Match 66.0%; Score 33; DB 2; Length 225;

Best Local Similarity 85.7%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||:|
Db 178 GHRELDK 184

RESULT 28

H95278

conserved hypothetical protein Sma0255 [imported] - Sinorhizobium meliloti (strain 1021)

C;Species: Sinorhizobium meliloti

C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: H95278

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe,

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: H95278

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 <KUR>

A;Cross-references: UNIPROT:Q930Q9; GB:AE006469; PIDN:AAK64794.1; PID:gl4523204; GSPDB:GN

A;Experimental source: strain 1021, megaplasmid pSymbA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaull, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: Sma0255

A;Genome: plasmid

Query Match 66.0%; Score 33; DB 2; Length 325;

Best Local Similarity 62.5%; Pred. No. 81;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
|||:|
Db 211 GHRVDDC 218

RESULT 29

AD2936

polymerase epsilon subunit Atu3090 [imported] - Agrobacterium tumefaciens (strain C58, D

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C;Accession: AD2936

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gallet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan,

Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I.

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AD2936

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-326 <KUR>

A;Cross-references: UNIPROT:Q9UBCG; GB:AE008689; PIDN:AAL43906.1; PID:gl7741456; GSPDB:GN

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu3090

A;Map position: linear chromosome

Query Match 66.0%; Score 33; DB 2; Length 326;

Best Local Similarity 62.5%; Pred. No. 81;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
|||:|
Db 214 GHRVDDC 221

RESULT 30

C98346

hypothetical protein AGR_L 3437 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C;Species: Agrobacterium tumefaciens

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: C98346
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* strain C58
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C98346
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-326 <KUR>
A;Cross-references: UNIPROT:Q8UBC6; GB:AE007870; PIDN:AAK90293.1; PID:gl5160320; GSPDB:G98259
C;Genetics:
A;Gene: AGR L 3437
A;Map position: linear chromosome

Query Match 66.0%; Score 33; DB 2; Length 326;
Best Local Similarity 62.5%; Pred. No. 81;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
||| : |||
Db 214 GHRVDDC 221

RESULT 31
T52184
zinc transporter ZIP2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52184
R;Grotz, N.; Fox, T.; Connolly, E.; Park, W.; Guerinot, M.L.; Eide, D. Proc. Natl. Acad. Sci. U.S.A. 95, 7220-4, 1998
A;Title: Identification of a family of zinc transporter genes from Arabidopsis that represses growth of the pathogen *Agrobacterium tumefaciens*
A;Reference number: Z5114; MUID:9618566; PMID:9618566
A;Accession: T52184
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-353 <GRO>
A;Cross-references: UNIPROT:Q9LTH9; EMBL:AF033536; PIDN:AAC24198.1
A;Experimental source: strain Landsberg erecta
C;Genetics:
A;Gene: ZIP2
C;Function:
A;Description: involved in zinc uptake

Query Match 66.0%; Score 33; DB 2; Length 353;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
||| : |||
Db 320 GYKPLEC 327

RESULT 32
AB3025
methionine gamma-lyase mdeA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AB3025
R;Wood, D.W.; Stetubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, S.; Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB3025
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-427 <KUR>

A;Cross-references: UNIPROT:Q8U9C2; GB:AE008689; PIDN:AA444616.1; PID:gl7742238; GSPDB:G98259
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: mdeA
C;Superfamily: O-succinylhomoserine (thiol)-lyase

Query Match 66.0%; Score 33; DB 2; Length 427;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
||| : |||
Db 208 GHRPIAC 215

RESULT 33
G98259
methionine gamma-lyase (AJ000486) [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: G98259
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* strain C58
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G98259
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-427 <KUR>
A;Cross-references: UNIPROT:Q8U9C2; GB:AE007870; PIDN:AAK89601.1; PID:gl5159492; GSPDB:G98259
C;Genetics:
A;Gene: AGR L 2052
A;Map position: linear chromosome
C;Superfamily: O-succinylhomoserine (thiol)-lyase

Query Match 66.0%; Score 33; DB 2; Length 427;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
||| : |||
Db 208 GHRPIAC 215

RESULT 34
A70706
probable phoR protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: A70706
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70706
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-485 <COL>
A;Cross-references: UNIPROT:P71815; GB:Z80226; GB:AL123456; NID:g3261638; PIDN:CAB02401.1
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: phoR
C;Superfamily: envZ protein; sensor histidine kinase homology
C;Keywords: autophosphorylation; phosphohistidine; phosphoprotein
F;217-467/Domain: sensor histidine kinase homology <SHK>
F;259/Binding site: phosphate (His) (covalent) (by autophosphorylation) #status predicted

Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPDLC 8
|||:
Db 313 HRPDLC 319

RESULT 35
D82654
ankyrin-like protein XF1640 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: D82654
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A8215; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: D82654
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1058 <SIM>
A/Cross-references: UNIPROT:Q9PCW4; GB:AE003991; GB:AE003849; NID:g9106696; PIDN:AAF8444
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.; Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Probst, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh, Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaak, M.; Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, W.A.; da Silva, J.; da Silva, M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

Query Match 66.0%; Score 33; DB 2; Length 1058;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
|||:
Db 497 GHRPVD 502

RESULT 36
T14075
chitinase (EC 3.2.1.14) - yellow fever mosquito
C/Species: Aedes aegypti (yellow fever mosquito)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14075
R/de la Vega, H.; Specht, C.A.; Liu, Y.; Robbins, P.W.
Insect Mol. Biol. 7, 233-239, 1997
A/Title: Chitinaes are a multi-gene family in Aedes, Anopheles, and Drosophila.
A/Reference number: Z17872
A/Accession: T14075
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-1635
A/Cross-references: UNIPROT:O17412; EMBL:AF026492; NID:g2564720; PID:g2564721; PIDN:AA88
C/Genetics:
A/Gene: CHT2
A/Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 66.0%; Score 33; DB 2; Length 1635;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RPLDKC 8
|||:
Db 54 RPYDKC 59

RESULT 37
S46349
trans-activating transcription regulator - simian immunodeficiency virus SIVagm (isolate N; Alternate names: tat protein
C/Species: simian immunodeficiency virus SIVagm
A/Variety: isolate SAB-1
C/Date: 25-Dec-1994 #sequence_revision 14-Feb-1997 #text_change 20-Sep-1999
C/Accession: S46349
R/jin, M.J.; Hui, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V.M.; EMBO J. 13, 2935-2947, 1994
A/Title: Mosaic genome structure of simian immunodeficiency virus from West African green A/Reference number: S46335; MUID:94298785; PMID:8026477
A/Accession: S46349
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-73 <JIN>
A/Cross-references: EMBL:U04005; NID:g466229; PIDN:AAA21507.1; PID:g4662233
A/Experimental source: isolate SAB-1; sabaesus monkey
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
C/Genetics:
A/Gene: tat
C/Superfamily: AIDS trans-activating transcription regulator

Query Match 64.0%; Score 32; DB 2; Length 73;
Best Local Similarity 71.4%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HRPDLC 8
|||:
Db 20 HRPDLC 26

RESULT 38
T17674
hypothetical protein A184L - Chlorella virus PBCV-1
C/Species: Chlorella virus PBCV-1
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T17674
R/Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A/Reference number: Z18806
A/Accession: T17674
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-116 <GRA>
A/Cross-references: UNIPROT:O84504; EMBL:U42580; NID:g4028896; PIDN:AAC96552.1
A/Experimental source: specific host Chlorella strain NC64
C/Genetics:
A/Note: al84L
C/Superfamily: Chlorella virus PBCV-1 hypothetical protein A184L

Query Match 64.0%; Score 32; DB 2; Length 116;
Best Local Similarity 57.1%; Pred. No. 47;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPDLC 8
|||:
Db 27 HRPYDEC 33

RESULT 39
E82256
conserved hypothetical protein VC0975 [imported] - Vibrio cholerae (strain N16961 serogroup C; Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: E82256

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406:477-483, 2000
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: E82256
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-189 <HEI>
 A;Cross-references: UNIPROT:Q9KTC7; GB:AE004179; GB:AE003852; NID:G9655432; PIDN:AAF9413
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VC0975
 A;Map position: 1

Query Match 64.0%; Score 32; DB 2; Length 189;
 Best Local Similarity 57.1%; Pred. No. 75;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
 Db 33 HKPLSRC 39
 |||||

RESULT 40

B71305
 hypothetical protein TP0608 - syphilis spirochete
 C;Species: *Treponema pallidum* subsp. *pallidum* (syphilis spirochete)
 C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C;Accession: B71305
 R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; MCD
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A>Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
 A;Reference number: A71250; MUID:98332770; PMID:9665876
 A;Accession: B71305
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-296 <COL>
 A;Cross-references: UNIPROT:O83617; GB:AE001235; GB:AE000520; NID:G3322893; PIDN:AAC6558
 A;Experimental source: strain Nichols
 C;Genetics:
 A;Gene: TP0608
 C;Superfamily: syphilis spirochete hypothetical protein TP0608

Query Match 64.0%; Score 32; DB 2; Length 296;
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
 Db 16 GHKPLTWC 23
 |||||

Search completed: June 1, 2005, 11:52:54
 Job time : 27.6 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 11:40:35 ; Search time 120 seconds
(without alignments)
34.139 Million cell updates/sec

Title: US-09-424-940A-2
Perfect score: 50
Sequence: 1 GHRPLDKC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	84.0	377	2 Q99FX0	Q99fx0 human papill
2	41	82.0	31	1 FIBB_CANFA	P02677 canis famil
3	41	82.0	491	1 FIBB_HUMAN	P02675 homo sapien
4	40	80.0	182	2 Q9LFM1	Q9lfm1 arabidopsis
5	40	80.0	246	2 Q7VSA4	Q7vsa4 bordetella
6	40	80.0	246	2 Q7WQ76	Q7wq76 bordetella
7	40	80.0	256	2 Q7WC72	Q7wc72 bordetella
8	39	78.0	135	2 Q8PKD6	Q8pkd6 xanthomonas
9	39	78.0	219	2 Q8FP29	Q8fp29 corynebacte
10	39	78.0	286	2 Q940Z1	Q940z1 arabidopsis
11	39	78.0	725	2 Q9LNA3	Q9lna3 arabidopsis
12	39	78.0	3207	2 Q8MWQ3	Q8mwq3 plasmodium
13	39	78.0	3287	2 Q8T326	Q8t326 plasmodium
14	38	76.0	50	2 Q9E8F8	Q9e8f8 porcine ade
15	38	76.0	50	2 Q9E8G2	Q9e8g2 porcine ade
16	38	76.0	308	2 Q7XDX0	Q7xdx0 oryza sativ
17	38	76.0	401	2 Q8RUP6	Q8rup6 oryza sativ
18	38	76.0	513	2 Q7XC43	Q7xc43 oryza sativ
19	38	76.0	513	2 Q9AY56	Q9ay56 oryza sativ
20	38	76.0	517	2 Q6DDT4	Q6ddt4 xenopus lae
21	38	76.0	517	2 Q6DFQ8	Q6dfq8 xenopus tro
22	38	76.0	626	2 Q84QX6	Q84qx6 oryza sativ
23	37	74.0	82	2 Q9PFF7	Q9pff7 xylella fas
24	37	74.0	279	2 Q8H2P3	Q8h2p3 oryza sativ
25	37	74.0	404	2 Q9VA50	Q9va50 drosophila
26	37	74.0	477	2 Q6YQZ6	Q6yqz6 caenorhabdi
27	37	74.0	477	2 Q7JBE9	Q7jbe9 caenorhabdi
28	37	74.0	490	2 Q09937	Q09937 caenorhabdi
29	37	74.0	490	2 Q86G19	Q86gi9 caenorhabdi
30	37	74.0	495	2 Q7JPF0	Q7jpf0 caenorhabdi
31	37	74.0	518	2 Q9S149	Q9s149 arabidopsis

32	37	74.0	575	2	Q96989	O96989 drosophila
33	37	74.0	591	1	YD72_MYCPN	P75409 mycoplasma
34	36	72.0	58	2	Q8MV72	Q8mv72 myxine glut
35	36	72.0	159	2	Q8E1G4	Q8e1g4 streptococc
36	36	72.0	159	2	Q8E6Y1	Q8e6y1 streptococc
37	36	72.0	201	2	Q92XY9	Q92xy9 rhizobium m
38	36	72.0	238	2	Q7MTW3	Q7mtw3 porphyromon
39	36	72.0	240	2	Q8UI44	Q8ui44 agrobacteri
40	36	72.0	246	2	Q8R328	Q8r328 mus musculu
41	36	72.0	260	2	Q8BJP7	Q8bjp7 mus musculu
42	36	72.0	260	2	Q8BUZ2	Q8buz2 mus musculu
43	36	72.0	265	2	Q8BYE9	Q8bye9 mus musculu
44	36	72.0	268	2	Q6TGR2	Q6tgr2 cryptococcu
45	36	72.0	385	2	Q9CS12	Q9cs12 mus musculu

ALIGNMENTS

RESULT 1
Q99FX0
ID Q99FX0 PRELIMINARY; PRT; 377 AA.
AC Q99FX0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative regulatory protein E2.
OS Human papillomavirus type 84.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=150546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21066735; PubMed=11145894; DOI=10.1006/viro.2000.0716;
RA Terai M., Burk R.D.;
RT "Complete nucleotide sequence and analysis of a novel human
RT papillomavirus (HPV 84) genome cloned by an overlapping PCR method.";
RL Virology 279:109-115(2001).
DR EMBL; AF293960; AAK0274.1; -.
DR HSSP; P06790; IP9F.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006275; P:regulation of DNA replication; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000427; E2_C.
DR InterPro; IPR001866; E2_N.
DR Pfam; PF00511; PPV_E2_C; 1.
DR Pfam; PF00508; PPV_E2_N; 1.
DR ProDom; PD000672; E2_C; 1.
DR ProDom; PD000678; E2_N; 1.
SQ SEQUENCE 377 AA; 43000 MW; 71FC5F656143A674 CRC64;

Query Match 84.0%; Score 42; DB 2; Length 377;
Rest Local Similarity 75.0%; Pred.No. 9.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
Db 265 GHRPVDSC 272

RESULT 2
FIBB_CANFA
ID FIBB_CANFA STANDARD; PRT; 31 AA.
AC P02677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN Name=FGB;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76081726; PubMed=1198547; DOI=10.1016/0049-3848(75)90106-1;
 RA Birken S., Wilner G.D., Canfield R.E.;
 RT "Studies of the structure of canine fibrinogen.";
 RL Thromb. Res. 7:599-610(1975).
 RN [2]
 RP SEQUENCE OF 1-19.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 RN [3]
 RP SEQUENCE OF 1-19.
 RX MEDLINE=6906367; PubMed=5727635;
 RA Krajewski T., Blomback B.;
 RT "The location of tyrosine-O-sulphate in fibrinopeptides.";
 RL Acta Chem. Scand. 22:1339-1346(1968).
 CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
 CC (alpha, beta and gamma), linked to each other by disulfide bonds.
 CC -1- PM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 DR PIR; B94308; A05297.
 DR InterPro: IPR002181; Fibrinogen C.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
 KW Blood coagulation; Direct protein sequencing; Plasma; Sulfation.
 FT PEPTIDE 1 19 Fibrinopeptide B.
 FT CHAIN 20 >31 Fibrinogen beta chain.
 FT MOD_RES 2 2 Sulfotyrosine (partial).
 FT MOD_RES 3 3 Sulfotyrosine.
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3731 MW; A043727257698156 CRC64;
 Query Match 82.0%; Score 41; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1-2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db 20 GHRPLDK 26
 RESULT 3
 FIBB_HUMAN STANDARD; PRT; 491 AA.
 AC P02675;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
 GN Names-FGB;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91344740; PubMed=2102623;
 RA Chung D.W., Harris J.E., Davie E.W.;
 RT "Nucleotide sequences of the three genes coding for human
 RT fibrinogen.";
 RL Adv. Exp. Med. Biol. 281:39-48(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83283433; PubMed=6688356;
 RA Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;
 RT "Characterization of complementary deoxyribonucleic acid and genomic

RT deoxyribonucleic acid for the beta chain of human fibrinogen.";
 RL Biochemistry 22:3244-3250(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Chung D.W., Harris J.E., Davie E.W.;
 RT "Nucleotide sequences of the three genes coding for human
 RT fibrinogen.";
 RL (In) Liu C.Y., Chien S. (eds.);
 RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48, Plenum
 RL Press, New York (1991).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS SER-100; HIS-170; LEU-265 AND
 RP LYS-478.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattlesNP, NHLBI HL66682 program for genomic applications, UW-
 RT FRCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RT structural variants.";
 RL (In) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [6]
 RP SEQUENCE OF 31-491.
 RX MEDLINE=79124640; PubMed=420779;
 RA Watt K.W.K., Takagi T., Doolittle R.F.;
 RT "Amino acid sequence of the beta chain of human fibrinogen.";
 RL Biochemistry 18:68-76(1979).
 RN [7]
 RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.
 RX MEDLINE=76225080; PubMed=936108; DOI=10.1016/0049-3848(76)90245-0;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
 RL Thromb. Res. 8:639-658(1976).
 RN [8]
 RP SEQUENCE OF 1-38 FROM N.A.
 RX MEDLINE=87146483; PubMed=3029722;
 RA Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z.,
 RA Marguerie G.;
 RT "Characterization of the 5'-flanking region for the human fibrinogen
 RT beta gene.";
 RL Nucleic Acids Res. 15:1615-1625(1987).
 RN [9]
 RP SEQUENCE OF 31-44.
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
 RT "Studies on fibrinopeptides from primates.";
 RL Acta Chem. Scand. 19:1788-1789(1965).
 RN [10]
 RP REVIEW, AND DISULFIDE BONDS.
 RX MEDLINE=83254370; PubMed=6575689;
 RA Henschen A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen.";
 RL Ann. N. Y. Acad. Sci. 408:28-43(1983).
 RN [11]
 RP DISULFIDE BONDS.
 RX MEDLINE=77245999; PubMed=891553;
 RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
 RT "Primary structure of human fibrinogen. Characterization of disulfide-
 RT containing cyanogen-bromide fragments.";
 RL Eur. J. Biochem. 77:595-610(1977).
 RN [12]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin.";
 RL (In) Magnusson S., Ottesen M., Foltmann B., Dano K., Neurath H.
 RL (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).

[13]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RL Annu. Rev. Biochem. 53:195-229 (1984).
 [14]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
 RX MEDLINE=97472408; PubMed=9332333; DOI=10.1038/38947;
 RA Spraggon G., Everse S.J., Doolittle R.F.;
 RL "Crystal structures of fragment D from human fibrinogen and its
 crosslinked counterpart from fibrin.";
 Nature 389:455-462 (1997).
 [15]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
 RX MEDLINE=98292399; PubMed=9628725; DOI=10.1021/b19804129;
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RL "Crystal structure of fragment double-D from human fibrin with two
 different bound ligands.";
 Biochemistry 37:8637-8642 (1998).
 [16]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 164-491.
 RX MEDLINE=99175089; PubMed=10074346; DOI=10.1021/b1982626w;
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RL "Conformational changes in fragments D and double-D from human
 fibrin(logen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 Biochemistry 38:2941-2946 (1999).
 [17]
 RP INTERACTION WITH FBLN1.
 RX MEDLINE=95370284; PubMed=7642629; DOI=10.1074/jbc.270.33.19458;
 RA Tran H., Tanaka A., Litvinovich S.V., Medved L.V., Haudenschild C.C.,
 RA Argraves W.S.;
 RL "The interaction of fibulin-1 with fibrinogen. A potential role in
 hemostasis and thrombolysis.";
 J. Biol. Chem. 270:19458-19464 (1995).
 [18]
 RP VARIANT BALTIMORE-2 LYS-478.
 RX MEDLINE=89058942; PubMed=3194892; DOI=10.1016/0049-3848(88)90096-5;
 RA Schmelzer C.H., Ebert R.F., Bell W.R.;
 RL "A polymorphism at B beta 448 of fibrinogen identified during
 structural studies of fibrinogen Baltimore II.";
 Thromb. Res. 52:173-177 (1988).
 [19]
 RP VARIANT ISE ARG-45.
 RX MEDLINE=91208409; PubMed=2018836;
 RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
 RA Asakura S., Shirakawa S.;
 RL "A new congenital abnormal fibrinogen Ise characterized by the
 replacement of B beta glycine-15 by cysteine.";
 Blood 77:1958-1963 (1991).
 [20]
 RP VARIANT NAPLES THR-98.
 RX MEDLINE=92340664; PubMed=1634610;
 RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
 RL "Molecular basis of fibrinogen Naples associated with defective
 thrombin binding and thrombophilia. Homozygous substitution of B beta
 68 Ala-->Thr.";
 J. Clin. Invest. 90:238-244 (1992).
 [21]
 RP VARIANTS IJMUIDEN CVS-44 AND NIJMEGEN CVS-74.
 RX MEDLINE=92228809; PubMed=1565641;
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
 RA Kerst A.F.J.A., Lord S.T.;
 RL "Abnormal fibrinogens IJMuiden (B beta Arg14-->Cys) and Nijmegen (B
 beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
 complexes.";
 Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482 (1992).
 [22]
 RP VARIANT NEW YORK-1 39-GLY--LEU-102 DEL.
 RX MEDLINE=85157605; PubMed=3156856;
 RA Liu C.Y., Koehn J.A., Morgan P.J.;
 RL "Characterization of fibrinogen New York 1. A dysfunctional fibrinogen
 with a deletion of B beta(9-72) corresponding exactly to exon 2 of the

gene.";
 J. Biol. Chem. 260:4390-4396 (1985).
 [23]
 RP VARIANTS GLU-2; LEU-265 AND LYS-478.
 RX MEDLINE=99318093; PubMed=10391209; DOI=10.1038/10290;
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RL "Characterization of single-nucleotide polymorphisms in coding regions
 of human genes.";
 Nat. Genet. 22:231-238 (1999).
 [24]
 RP ESPATUM.
 RX PubMed=10545957;
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RL "Nat. Genet. 23:373-373 (1999).
 [25]
 RP VARIANTS CONGENITAL AFIBRINOGENEMIA ARG-383 AND ASP-430.
 RX MEDLINE=20129589; PubMed=10666208;
 RA Duga S., Asselta R., Santagostino E., Zeinali S., Simoncic T.,
 RA Malcovati M., Mannucci P.M., Turchini M.L.;
 RL "Missense mutations in the human beta fibrinogen gene cause congenital
 afibrinogenemia by impairing fibrinogen secretion.";
 Blood 95:1336-1341 (2000).
 [26]
 RP VARIANT CONGENITAL AFIBRINOGENEMIA CYS-196.
 RX MEDLINE=21361164; PubMed=11468164; DOI=10.1182/blood.V98.3.661;
 Query Match 82.0%; Score 41; DB 1; Length 491;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db 45 GHRPLDK 51
 RESULT 4
 Q9LFM1 PRELIMINARY; PRT; 182 AA.
 ID Q9LFM1
 AC Q9LFM1
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein F2111_250.
 GN Name=F2111_250;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Rukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Peters S.A., van Staveren M., Dirks W., Stiekema W.,
 RA Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL360314; CAB96671.1; -
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004672; F:protein kinase activity; IEA.
 DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR ProDom; PD000001; Prot_kinase; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 182 AA; 20577 MW; F485F31EA802BEFC CRC64;

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Query Match      80.0%; Score 40; DB 2; Length 182;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
DB 175 GHRDMDKC 182

RESULT 5
ID Q7VSA4 PRELIMINARY; PRT; 246 AA.
AC Q7VSA4
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable transcriptional regulator.
GN OrderedLocusNames=BP0533;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Collins M., Cronin A., Davis P., Doggett J.,
RA Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagsels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL: BX640412; CAB44861.1; -.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR005471; HTH_ICLR.
DR SMART: SM00346; HTH_ICLR; 1.
DR Complete proteome: DNA-binding; Transcription;
DR Transcription regulation.
SQ SEQUENCE 246 AA; 26265 MW; A3060D263DE488F6 CRC64;

Query Match      80.0%; Score 40; DB 2; Length 246;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
DB 129 GGRPLDKC 136

RESULT 6
ID Q7WQ76 PRELIMINARY; PRT; 246 AA.
AC Q7WQ76
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable transcriptional regulator.
GN OrderedLocusNames=BB0456;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Collins M., Cronin A., Davis P., Doggett J.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagsels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL: BX640412; CAB44861.1; -.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR005471; HTH_ICLR.
DR SMART: SM00346; HTH_ICLR; 1.
DR Complete proteome: DNA-binding; Transcription;
DR Transcription regulation.
SQ SEQUENCE 246 AA; 26265 MW; A3060D263DE488F6 CRC64;

Query Match      80.0%; Score 40; DB 2; Length 246;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
DB 129 GGRPLDKC 136

RESULT 7
ID Q7WC72 PRELIMINARY; PRT; 256 AA.
AC Q7WC72
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable transcriptional regulator.
GN OrderedLocusNames=BP0456;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Collins M., Cronin A., Davis P., Doggett J.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagsels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL: BX640424; CAB36039.1; -.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR005471; HTH_ICLR.
DR SMART: SM00346; HTH_ICLR; 1.
DR Complete proteome:
DR Transcription regulation.
SQ SEQUENCE 256 AA; 27270 MW; CF6B59887A9A962A CRC64;

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Query Match      80.0%; Score 40; DB 2; Length 256;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
Db 139 GGRPLDKC 146

RESULT 8
Q8PKD6 PRELIMINARY; PRT; 135 AA.
AC Q8PKD6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein XAC2239.
GN OrderedLocusNames=XAC2239;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furian L.R.,
RA Quaggio R.B., Monteiro-Vicorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chambergro F., Ciapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C. de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White P.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE011861; ANM37092.1; -.
KW Complete proteome.
SQ SEQUENCE 135 AA; 14910 MW; 9BC4F646126255EA CRC64;

Query Match      78.0%; Score 39; DB 2; Length 135;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
Db 79 GHRPLEC 86

RESULT 9
Q8FP29 PRELIMINARY; PRT; 219 AA.
AC Q8FP29;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative ankryrin repeat-containing protein.
GN OrderedLocusNames=CE1961;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314;

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RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori I.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RL Genome Res. 13:1572-1579(2003).
DR EMBL; AP005220; BAC18771.1; -.
DR HSP; P25963; IYKN.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank; 3.
DR PRINTS; PR01415; ANKIRIN.
DR SMART; SM00248; ANK; 3.
DR PROSITE; PS50088; ANK_REPEAT; 2.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW Complete proteome.
SQ SEQUENCE 219 AA; 23415 MW; 3A6CB06B3FD59E28 CRC64;

Query Match      78.0%; Score 39; DB 2; Length 219;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
Db 43 GHRPVNRC 50

RESULT 10
Q940Z1 PRELIMINARY; PRT; 266 AA.
AC Q940Z1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AC1919520/F18014.36.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsais.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
RA Hayaishizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayaishizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY052347; AAK96539.1; -.
DR EMBL; AY061908; AAL31235.1; -.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR008940; Prenyl_trans.
DR Pfam; PF01535; PPR; 6.
DR TIGRFAMs; TIGR00756; PPR; 4.
SQ SEQUENCE 266 AA; 29615 MW; 46CB125C324A8A30 CRC64;

Query Match      78.0%; Score 39; DB 2; Length 266;
Best Local Similarity 75.0%; Pred. No. 26;

```

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
||:|||||
Db 96 GHRPDDKC 103

RESULT 11

ID Q9LN43 PRELIMINARY; PRT; 725 AA.
AC Q9LN43;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE F18014.27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bei Q., Chin C., Chioi J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chioi J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
RA Shinn P., Altafi H., Bei B., Chin C., Chioi J., Choi E., Conn L.,
RA Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
RA Ecker J.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC025808; AAF79432.1; -.
DR PIR; A86328; A86328.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002197; HTH_Fis.
DR InterPro; IPR002885; PPR.
DR Pfam; PF01535; PPR; 8.
DR PRINTS; PR01590; HTHFIS.
DR TIGRfam; TIGR00756; PPR; 7.
SQ SEQUENCE 725 AA; 82535 MW; 9218477745237BFA CRC64;

Query Match 78.0%; Score 39; DB 2; Length 725;
Best Local Similarity 75.0%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
||:|||||
Db 555 GHRPDDKC 562

RESULT 12

Q8MWQ3 PRELIMINARY; PRT; 3207 AA.
AC Q8MWQ3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Erythrocyte membrane protein 1 (Fragment).
GN Name=var;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22072568; PubMed=12076777; DOI=10.1016/S0166-6851(02)00080-4;
RA Salanti A., Jensen A.T.R., Zornig H.D., Staalssoe T., Joergensen L.,
RA Nielsen M.A., Khattab A., Arnot D.E., Klinkert M.Q., Hviid L.,
RA Theander T.G.;
RT "A sub-family of common and highly conserved Plasmodium falciparum var
RT genes";
RL Mol. Biochem. Parasitol. 122:111-115(2002).
DR EMBL; AF411601; AAM55194.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005539; F:glycosaminoglycan binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008602; Duffy binding.
DR InterPro; IPR004258; PfEMP.
DR Pfam; PF05424; Duffy binding; 1.
DR Pfam; PF03011; PFEMP_1
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1 1
FT NON_TER 3207 3207
SQ SEQUENCE 3207 AA; 374119 MW; EC104D72B0866ESF CRC64;

Query Match 78.0%; Score 39; DB 2; Length 3207;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPDLKC 8
||:|||||
Db 2797 HRPDLKC 2803

RESULT 13

ID Q8T326 PRELIMINARY; PRT; 3287 AA.
AC Q8T326;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PFEMP1 (Fragment).
GN Name=TWI80var2;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TW180;
RX MEDLINE=2197235; PubMed=11930336;
RA Rowe J.A., Kyes S.A., Rogerson S.J., Babiker H.A., Raza A.;
RT "Identification of a conserved Plasmodium falciparum var gene
RT implicated in malaria in pregnancy";
RL J. Infect. Dis. 185:1207-1211(2002).
DR EMBL; AJ420411; CAD20867.1; -.
DR GO; GO:0005539; F:glycosaminoglycan binding; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF03011; PFEMP_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 3287 3287
SQ SEQUENCE 3287 AA; 383553 MW; 58F8F866FC244536 CRC64;

Query Match 78.0%; Score 39; DB 2; Length 3287;
 Best Local Similarity 85.7%; Pred. No. 3 Se+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
 Db 2872 HHPLDKC 2878

RESULT 14

Q9E8F8 PRELIMINARY; PRT; 50 AA.
 AC Q9E8F8
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE ORF4.
 OS Porcine adenovirus 5.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=45370;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HNF-70;
 RX MEDLINE=20416365; PubMed=10958982; DOI=10.1016/S0168-1702(00)00157-X;
 RA Tuboly T., Nagy E.;
 RT "Sequence analysis and deletion of porcine adenovirus serotype 5 E3 region."
 RL Virus Res. 68:109-117(2000).
 DR EMBL; AF186622; AAG10234.1;
 SQ SEQUENCE 50 AA; 5589 MW; 02DDECC59A16F3F0 CRC64;

Query Match 76.0%; Score 38; DB 2; Length 50;
 Best Local Similarity 85.7%; Pred. No. 7.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
 Db 44 HRPLDTC 50

RESULT 15

Q9E8G2 PRELIMINARY; PRT; 50 AA.
 AC Q9E8G2
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE ORF4.
 OS Porcine adenovirus 5.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=45370;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HNF-61;
 RX MEDLINE=20416365; PubMed=10958982; DOI=10.1016/S0168-1702(00)00157-X;
 RA Tuboly T., Nagy E.;
 RT "Sequence analysis and deletion of porcine adenovirus serotype 5 E3 region."
 RL Virus Res. 68:109-117(2000).
 DR EMBL; AF186621; AAG10229.1;
 SQ SEQUENCE 50 AA; 5521 MW; D546CCC59A16F417 CRC64;

Query Match 76.0%; Score 38; DB 2; Length 50;
 Best Local Similarity 85.7%; Pred. No. 7.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
 Db 44 HRPLDTC 50

RESULT 16

Q7XDX0 PRELIMINARY; PRT; 308 AA.
 AC Q7XDX0
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Contains similarity to ribosomal protein.
 GN ORFNames=OSUNBa0076M18.6;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice chromosome 10."
 RL Science 300:1566-1569(2003).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017100; AAP54021.1;
 DR Gramene; Q7XDX0;
 DR GO; GO:0003735; F:Structural constituent of ribosome; IEA.
 DR InterPro; IPR008966; Adhes_bact.
 DR InterPro; IPR006912; DUF635.
 DR Pfam; PF04827; DUF635; 1.
 KW Ribosomal protein.
 SQ SEQUENCE 308 AA; 35289 MW; 66961D35FFE71788 CRC64;

Query Match 76.0%; Score 38; DB 2; Length 308;
 Best Local Similarity 75.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHPLDKC 8
 Db 120 GHSPLQKC 127

RESULT 17

Q8RUP6 PRELIMINARY; PRT; 401 AA.
 AC Q8RUP6
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE P0703B11.15 protein (P0485B12.7 protein).
 GN Names=P0703B11.15; Synonyms=P0485B12.7;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12447436; DOI=10.1038/nature01184;
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Katayose Y.,
 RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijishita S., Honda M., Ichikawa Y., Iiduma A., Iijima M., Ikeda M.,
 RA Ikano M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machita K., Machihara T., Mizuno H., Mizubayashi T., Mukai Y.,

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RA Nagasaki H., Nakashima M., Nakama Y., Nakanishi Y., Nakamura M.,
RA Naniki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003302; BAB852296.1; -.
DR EMBL; AP003348; BAB86477.1; -.
DR Gramene; Q8RUP6; -.
DR InterPro; IPR006912; DUF635.
DR Pfam; PF04827; DUF635; 1.
SQ SEQUENCE 401 AA; 46131 MW; 9BF7BA7748970E05 CRC64;

Query Match 76.0%; Score 38; DB 2; Length 401;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
Db 120 GHSPLQKC 127

RESULT 18
ID Q7XC43 PRELIMINARY; PRT; 513 AA.
AC Q7XC43;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN ORFNames=OSJNBa0027P10.13;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017120; AAF55032.1; -.
DR Gramene; Q7XC43; -.
DR InterPro; IPR008966; Adhes bact.
DR InterPro; IPR006912; DUF635.
DR Pfam; PF04827; DUF635; 1.
KW Hypothetical protein.
SQ SEQUENCE 513 AA; 57948 MW; C9EE96E9ABA816BB CRC64;

Query Match 76.0%; Score 38; DB 2; Length 513;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
Db 120 GHSPLQKC 127

RESULT 19
ID Q9AY56 PRELIMINARY; PRT; 513 AA.
AC Q9AY56;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein OSJNBa0027P10.13.

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GN Name=OSJNBa0027P10.13;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Hsiao J.,
RA Ziemann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E., Craven B.,
RA Khalak H., Feldblyum T.V., Quackenbush J., White O., Salzberg S.L.,
RA Fraser C.M.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084763; AAG60187.1; -.
DR Gramene; Q9AY56; -.
DR InterPro; IPR008966; Adhes bact.
DR InterPro; IPR006912; DUF635.
DR Pfam; PF04827; DUF635; 1.
KW Hypothetical protein.
SQ SEQUENCE 513 AA; 57948 MW; C9EE96E9ABA816BB CRC64;

Query Match 76.0%; Score 38; DB 2; Length 513;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
Db 120 GHSPLQKC 127

RESULT 20
Q6DDT4
ID Q6DDT4 PRELIMINARY; PRT; 517 AA.
AC Q6DDT4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Apex2-prov protein.
GN Name=apex2-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077433; AAH77433.1; -;
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR InterPro; IPR000097; Apendonclisel.
DR InterPro; IPR004808; ExoIII xth.
DR InterPro; IPR051135; Exo endo phos.
DR Pfam; PF03372; Exo endo phos; 1.
DR Pfam; PF06839; zf-GRF; 1.
DR TIGRFAMs; TIGR00633; xth; 1.
DR PROSITE; PS00726; AP_NUCLEASE_F1.1; 1.
SQ SEQUENCE 517 AA; 57726 MW; 92C457CB579EC530 CRC64;
Query Match 76.0%; Score 38; DB 2; Length 517;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 HRPLDKC 8
Db 188 HRPLDHC 194
RESULT 21
ID Q6DF08 PRELIMINARY; PRT; 517 AA.
AC Q6DF08;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Apex2-prov protein.
GN Name=apex2-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076676; AAH76676.1; -;
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR InterPro; IPR000097; Apendonclisel.
DR InterPro; IPR004808; ExoIII xth.
DR InterPro; IPR051135; Exo endo phos.
DR InterPro; IPR010666; ZF-GRF.
DR Pfam; PF03372; Exo endo phos; 1.
DR Pfam; PF06839; zf-GRF; 1.
DR TIGRFAMs; TIGR00633; xth; 1.
DR PROSITE; PS00726; AP_NUCLEASE_F1.1; 1.
SQ SEQUENCE 517 AA; 57351 MW; 57B2062D0E8D27F CRC64;
Query Match 76.0%; Score 38; DB 2; Length 517;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 HRPLDKC 8
Db 188 HRPLDHC 194
RESULT 22
ID Q84QX6 PRELIMINARY; PRT; 626 AA.
AC Q84QX6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein OSUNBA0093113.9.
GN Name=OSUNBA0093113.9;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RN SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton I.L., Taitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosch D.W., Tallon L.J., Koo H., Ziemann V., Heiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC097279; AAP04202.1; -;
DR Gramene; Q84QX6; -;
KW Hypothetical protein.
SQ SEQUENCE 626 AA; 71611 MW; C8B6FE7F24438418 CRC64;
Query Match 76.0%; Score 38; DB 2; Length 626;
Best Local Similarity 75.0%; Pred. No. 99;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GHRPLDKC 8
Db 307 GHSPLQKC 314
RESULT 23
ID Q9PFF7 PRELIMINARY; PRT; 82 AA.
AC Q9PFF7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=Xf0702;
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 OC NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9a5c;
 RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Faccinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuranae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchioka M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa."
 RL Nature 406:151-159(2000).
 DR EMBL: AE003913; AAP83512.1; -;
 DR PIR; D82773; D82773.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 82 AA; 9067 MW; BCD6C81A85EA7ED CRC64;
 Query Match 74.0%; Score 37; DB 2; Length 82;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GHRPLDKC 8
 Db 59 GHSPLGKC 66
 ID Q8H2P3 PRELIMINARY; PRT; 279 AA.
 AC Q8H2P3
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE Hypothetical protein QJ1138_B05.110.
 GN Names=QJ1138_B05.110;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Sasaki T., Matsumoto T., Katayose Y.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005486; BAC16191.1; -;

DR Gramene; Q8H2P3; -;
 KW Hypothetical protein.
 SQ SEQUENCE 279 AA; 29739 MW; FEA38B9FE8AC748D CRC64;
 Query Match 74.0%; Score 37; DB 2; Length 279;
 Best Local Similarity 75.0%; Pred. No. 68;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GHRPLDKC 8
 Db 189 GGRPVDKC 196
 ID Q9VA50 PRELIMINARY; PRT; 404 AA.
 AC Q9VA50
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CG31013-PA.
 GN ORFNames=CG31013;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
 RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck C.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celisner S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN EMBL: AE003774; AAF57073.2; -;
DR FlyBase; PFG0051015; PH4-alpha-PV.
DR GO; GO:0016706; P:oxidoreductase activity, acting on paired d. . .; IEA.
DR GO; GO:0019538; P:protein metabolism; IEA.
DR InterPro; IPR005123; 2OG-FeII Oxy.
DR InterPro; IPR006620; Pro 4 hvd alph.
DR Pfam; PF03171; 2OG-FeII_Oxy; 1.
DR SMART; SM00702; P4HC; 1.
SQ SEQUENCE 404 AA; 46606 MW; 09330C64B0769F05 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 404;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 20 GHRPLEK 26

RESULT 26
Q6YGE6 PRELIMINARY; PRT; 477 AA.
AC Q6YGE6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE KVS-2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sesti F.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN EMBL: AY150829; AAN75511.1; -;

DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005249; P:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR001622; Ion trans.
DR InterPro; IPR003971; Kv9 channel.
DR InterPro; IPR003968; Kv channel.
DR InterPro; IPR003091; K channel.
DR InterPro; IPR003131; K tetra.
DR InterPro; IPR005820; M channel_nlg.
DR Pfam; PF02214; K tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01494; KV9CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 477 AA; 53396 MW; 05FA5DF39C58B292 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 477;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HRPLDKC 8
Db 145 HRPLDVC 151

RESULT 27
Q7JPE9 PRELIMINARY; PRT; 477 AA.
AC Q7JPE9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE K (Potassium) voltage-gated sensory channel subunit protein 1, isoform
DE C.
GN Name=kvs-1; ORFNames=C53C9.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid C53C9.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [6]

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RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RN Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RN Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
[8]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U28734; AAK30209.1; -.
DR WormPep; C53C9.3c; CE36283.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K-channel pore.
DR InterPro; IPR003971; Kv9_channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR005820; M-channel_nlg.
DR Pfam; PF00520; Ion trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01494; KV9CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 477 AA; 53428 MW; 336CCDCP6D610C22 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 477;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
Db 145 HRPLDVC 151

RESULT 28
Q09937 PRELIMINARY; PRT; 490 AA.
AC Q09937;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE K (Potassium) voltage-gated sensory channel subunit protein 1, isoform a.
DE
GN Name=kvs-1; ORFNames=C53C9.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL MEDLINE=99069613; PubMed=9851916;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid C53C9.";
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RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RA Waterston R.;
RN Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RN Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RN Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RN Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RN Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
[8]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U28734; AAB52604.3; -.
DR PIR; T15829; T15829.
DR HSP; Q54397; IBL8.
DR WormBase; WBGene00002242; kvs-1.
DR WormPep; C53C9.3a; CE34278.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K-channel pore.
DR InterPro; IPR003971; Kv9_channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR005820; M-channel_nlg.
DR Pfam; PF00520; Ion trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01494; KV9CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 490 AA; 54768 MW; A8346C293F93D15B CRC64;

Query Match 74.0%; Score 37; DB 2; Length 490;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
Db 145 HRPLDVC 151

RESULT 29
Q086G19 PRELIMINARY; PRT; 490 AA.
AC Q086G19;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE KVS-1.
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OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22552398; PubMed=12533541; DOI=10.1074/jbc.M212788200;
 RA Bianchi L., Kwok S.M., Driscoll M., Sesti F.;
 RT "A potassium channel-MiRP complex controls neurosensory function in
 Caenorhabditis elegans.";
 RL J. Biol. Chem. 278:12415-12424 (2003).
 DR EMBL; AF541979; AAC65852.1; -;
 DR HSSP; Q54397; 1BL8.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0008076; C: voltage-gated potassium channel complex; IEA.
 DR GO; GO:0005249; F: voltage-gated potassium channel activity; IEA.
 DR GO; GO:0006812; P: cation transport; IEA.
 DR GO; GO:0006813; P: potassium ion transport; IEA.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003971; Kv9_channel.
 DR InterPro; IPR003968; Kv_channel.
 DR InterPro; IPR003091; K_channel.
 DR InterPro; IPR003131; K_tetra.
 DR Pfam; PF00520; Ion trans; 1.
 DR Pfam; PF02214; K_tetra; 1.
 DR PRINTS; PR00169; KCHANNEL.
 DR PRINTS; PR01494; KV9CHANNEL.
 DR PRINTS; PR01491; KVCHANNEL.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 490 AA; 54737 MW; 9B362E2767CBB738 CRC64;
 Query Match 74.0%; Score 37; DB 2; Length 490;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 HRPDKC 8
 DB 145 HRPDVC 151
 RESULT 30
 Q7DPFO
 ID Q7DPFO PRELIMINARY; PRT; 495 AA.
 AC Q7DPFO;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created).
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE K (Potassium) voltage-gated sensory channel subunit protein 1, isoform
 DE b.
 GN Name=kvs-1; ORFNames=C53C9.3;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RG WormBase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Bentley D.;
 RT "The sequence of C. elegans cosmid C53C9.";
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;

RA Waterston R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U28734; AAR25654.1; -;
 DR WormBase; WBGene0002242; kvs-1.
 DR WormPep; C53C9.3b; CE30914.
 DR GO; GO:0016020; C: membrane; IEA.
 DR GO; GO:0008076; C: voltage-gated potassium channel complex; IEA.
 DR GO; GO:0005249; F: voltage-gated potassium channel activity; IEA.
 DR GO; GO:0006812; P: cation transport; IEA.
 DR GO; GO:0006813; P: potassium ion transport; IEA.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003971; Kv9_channel.
 DR InterPro; IPR003968; Kv_channel.
 DR InterPro; IPR003091; K_channel.
 DR InterPro; IPR003131; K_tetra.
 DR InterPro; IPR005820; M+channel_nlg.
 DR Pfam; PF00520; Ion trans; 1.
 DR Pfam; PF02214; K_tetra; 1.
 DR PRINTS; PR00169; KCHANNEL.
 DR PRINTS; PR01494; KV9CHANNEL.
 DR PRINTS; PR01491; KVCHANNEL.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 495 AA; 55244 MW; 278F3635A4D83D72 CRC64;
 Query Match 74.0%; Score 37; DB 2; Length 495;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 HRPDKC 8
 DB 150 HRPDVC 156
 RESULT 31
 Q9SI49
 ID Q9SI49 PRELIMINARY; PRT; 518 AA.
 AC Q9SI49;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative cytochrome P450.
 GN Name=At2g14100;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;

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RN
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Niernan W.C.,
RA Fraser C.M., Venter J.C.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN
[2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -(-) SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AC007197; AB25850.1; -.
DR PIR; B84514; B84514.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP450I.
DR InterPro; IPR001783; Lum_binding.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
DR PROSITE; PS00693; LUM_BINDING; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ
SEQUENCE 518 AA; 58814 MW; 221B94886F602F94 CRC64;
Query Match 74.0%; Score 37; DB 2; Length 518;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
Db 112 GHPPIDEC 119

RESULT 32
ID 096989 PRELIMINARY; PRT; 575 AA.
AC 096989;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE C3658-PA (CDC45L) (EG:BACR7A4.11 protein) (Pbgn0026143;cdc45l
DE protein) (L3D35753p)
GN Name=CDC45L; Synonyms=EG:BACR7A4.11; ORFNames=CG3658;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan M.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glisdek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,

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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lilang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426089; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Rettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN
[5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN
[6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RN Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN
[7]
RP SEQUENCE FROM N.A.
RX MEDLINE=99160479; PubMed=10051334;
RA Shaikh T.H., Gottlieb S., Sellinger B., Chen F., Roe B.A., Oakley R.J.,
RA Emanuel B.S., Budarf M.L.;
RT "Characterization of CDC45L: a gene in the 22q11.2 deletion region
RT expressed during murine and human development."
RL Mamm. Genome 10:322-326 (1999).
RN
[8]
RP SEQUENCE FROM N.A.
RA Papagiannakis G., Spanos L., Bolshakov V., Siden-Kiamos I., Louis C.;
RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

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[9]
RN RP SEQUENCE FROM N.A.
RA Benos P.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[10]
RN RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Friese E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.B., Rubin G.M., Ceiniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003419; AAF45579.1; -
DR EMBL; AF081540; AAD09003.1; -
DR EMBL; ALJ09630; CAB51681.1; -
DR EMBL; AY051861; AAK93285.1; -
DR IntAct; O96989; -
DR FlyBase; FBgn0026143; CDC45L.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0005556; C:pre-replicative complex; IPI.
DR GO; GO:0003682; F:chromatin binding; IDA.
DR GO; GO:0006277; P:DNA amplification; IBP.
DR InterPro; IPR003874; CDC45_like.
DR Pfam; PF02724; CDC45; 1.
SQ SEQUENCE 575 AA; 65890 MW; A58341D46DEPE618 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 575;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HRPLDKC 8
Db 101 HRPLDVC 107

RESULT 33
YD72 MYCPN STANDARD; PRT; 591 AA.
AC PY5409;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein WPN372 (A19_orf591).
GN OrderedLocNames=WPN372; ORFNames=MP464;
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
RA Himmelfreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA Hartmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000046; AAB96112.1; -
DR InterPro; IPR003898; Borpert_toxa.
DR Pfam; PF02917; Pertussis_S1; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 591 AA; 68057 MW; B958C85C9EBE29E90 CRC64;
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Query Match 74.0%; Score 37; DB 1; Length 591;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
Db 240 GENPLDKC 247

RESULT 34
Q8MVT2 PRELIMINARY; PRT; 58 AA.
ID Q8MVT2;
AC Q8MVT2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-tubulin 2 (Fragment).
GN Names=TUBA2;
OS Myxine glutinosa (Atlantic hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Myxiniinae; Myxine.
OX NCBI_TaxID=7769;
RN [1]
RP SEQUENCE FROM N.A.
RA Edvardsen R.B., Flat M., Tewari R., Jensen M.F., Seo H.C., Lehrach H.,
RA Reinhardt R., Chourrout D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF465689; AAM73994.1; -
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002452; Alphatubulin.
DR InterPro; IPR003008; Tubulin_FtsZ.
DR Pfam; PF00091; Tubulin; 1.
DR PRINTS; PR01162; ALPHATUBULIN.
KW GTP-binding.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 6375 MW; 0122F7B17D9D4B93 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 58;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 18 GHRPADK 24

RESULT 35
Q8E1G4 PRELIMINARY; PRT; 159 AA.
ID Q8E1G4;
AC Q8E1G4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcriptional regulator, Fur family.
GN OrderedLocNames=SAG0391;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolenay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
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RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014209; ANM99297.1; -.
DR TIGR; SAG0391; -.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002481; FUR.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF01475; FUR; 1.
DR ProDom; PD002003; FUR; 1.
DR Complete proteome.
KW SEQUENCE 159 AA; 18584 MW; 31FBA715A358C127 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 7 GHRPLD 12

RESULT 36.
Q8E6Y1 PRELIMINARY; PRT; 159 AA.
AC Q8E6Y1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein gbs0427.
GN OrderedLocustNames=gbs0427;
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangul L.,
RA Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL; AL766845; CAD46071.1; -.
DR Sagalib; gbs0427; -.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002481; FUR.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF01475; FUR; 1.
DR ProDom; PD002003; FUR; 1.
DR Complete proteome; Hypothetical protein.
KW SEQUENCE 159 AA; 18584 MW; 31FBA715A358C127 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 7 GHRPLD 12

RESULT 37
Q92XY9 PRELIMINARY; PRT; 201 AA.
ID Q92XY9
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Putative transcriptional regulator.
GN OSFNAMES=SMa2008;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymA megaplasmid.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001)
CC -i- SIMILARITY: Contains 1 HTH tetr-type DNA-binding domain.
DR EMBL; AE007296; AK65757.1; -.
DR PIR; C95399; C95399.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR001647; HTH_Tetr.
DR Pfam; PF00440; Tetr_N; 1.
DR PRINTS; PR00455; HTH_TETR.
KW Complete proteome; DNA-binding; Plasmid; Transcription;
KW Transcription regulation.
SQ SEQUENCE 201 AA; 21500 MW; 447E9B9BF63EF551 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 175 GHRPLD 180

RESULT 38
Q7MTW3 PRELIMINARY; PRT; 238 AA.
ID Q7MTW3
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=PGI818;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601(2003).
DR EMBL; AE017178; AAQ66816.1; -.
DR TIGR; PGI818; -.

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AC Q92XY9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative transcriptional regulator.
GN OSFNAMES=SMa2008;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymA megaplasmid.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001)
CC -i- SIMILARITY: Contains 1 HTH tetr-type DNA-binding domain.
DR EMBL; AE007296; AK65757.1; -.
DR PIR; C95399; C95399.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR001647; HTH_Tetr.
DR Pfam; PF00440; Tetr_N; 1.
DR PRINTS; PR00455; HTH_TETR.
KW Complete proteome; DNA-binding; Plasmid; Transcription;
KW Transcription regulation.
SQ SEQUENCE 201 AA; 21500 MW; 447E9B9BF63EF551 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 175 GHRPLD 180

RESULT 38
Q7MTW3 PRELIMINARY; PRT; 238 AA.
ID Q7MTW3
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=PGI818;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601(2003).
DR EMBL; AE017178; AAQ66816.1; -.
DR TIGR; PGI818; -.

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KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 238 AA; 26945 MW; DCA6C728CE6C8448 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 238;
Best Local Similarity 85.7%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
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Db 3 GHRPTDK 9

RESULT 39
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AC Q8UI44;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Atu0456.
GN OrderedLocusNames=Atu0456;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
C58."
RL Science 294:2317-2323(2001).
DR EMBL; AE009016; AAL41475.1; -.
DR PIR; AE2632; AE2632.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 240 AA; 27768 MW; 7B85FD4C723D616 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 240;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
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Db 144 HRPLKRC 150

RESULT 40
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AC Q8R328;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Apex2 protein.
GN Name=Apex2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=CZECH II; TISSUE=Mammary tumor;
RC Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026769; AH26769.1; -.
DR HSSP; P09030; IAKO.
DR MGD; MGI:1924872; Apex2.
DR GO; GO:0005743; C:mitochondrial inner membrane; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR000097; APendonclsel.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
SQ SEQUENCE 246 AA; 27389 MW; 194A6128F3CB1D8F CRC64;

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Query Match 72.0%; Score 36; DB 2; Length 246;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 2 HRPLDKC 8
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Db 201 HRPLDKC 207

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Search completed: June 1, 2005, 11:52:01
Job time : 122 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 11:41:40 ; Search time 28 seconds
(without alignments)
18.662 Million cell updates/sec

Title: US-09-424-940A-1

Perfect score: 41

Sequence: 1 GHRPLDK 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PTCUS COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	7	1	US-08-058-699-10
2	41	100.0	8	1	Sequence 10, Appl
3	41	100.0	10	2	US-08-058-699-11
4	41	100.0	20	4	Sequence 1, Appl
5	41	100.0	25	4	Sequence 6, Appl
6	41	100.0	28	1	US-10-142-935-4
7	41	100.0	28	1	US-08-486-135-12
8	41	100.0	28	1	US-08-470-152-12
9	41	100.0	28	2	US-08-468-964B-10
10	41	100.0	28	2	US-07-871-282A-10
11	41	100.0	28	2	US-08-290-853-33
12	41	100.0	28	3	US-08-253-678A-10
13	41	100.0	28	3	US-08-582-134B-10
14	41	100.0	30	2	US-08-170-299-10
15	41	100.0	31	1	US-08-290-853-35
16	41	100.0	31	1	US-08-472-535-9
17	41	100.0	31	1	US-08-484-774-9
18	41	100.0	31	3	US-08-266-178A-9
19	41	100.0	118	4	US-09-513-999C-4232
20	41	100.0	150	4	US-09-513-999C-4231
21	41	100.0	488	4	US-09-919-039-33
22	41	100.0	491	1	US-08-206-176-4
23	41	100.0	493	4	US-09-949-016-9617
24	36	87.8	10	4	US-10-142-935-9
25	36	87.8	15	4	US-10-142-935-8
26	36	87.8	20	4	US-10-142-935-5
27	36	87.8	74	4	US-09-248-796A-26425
			194	4	US-09-252-991A-23750

28	35	85.4	1203	4	US-09-799-875-5	Sequence 5, Appli
29	34	82.9	788	4	US-09-252-991A-28544	Sequence 28544, A
30	33	80.5	305	4	US-09-252-991A-28874	Sequence 28874, A
31	33	80.5	379	4	US-09-252-991A-28924	Sequence 28924, A
32	33	80.5	497	4	US-09-252-991A-22575	Sequence 22575, A
33	33	80.5	579	4	US-09-252-991A-30324	Sequence 30324, A
34	33	80.5	632	4	US-09-252-991A-24235	Sequence 24235, A
35	33	80.5	1020	4	US-09-252-991A-28870	Sequence 28870, A
36	32	78.0	266	4	US-09-252-991A-30538	Sequence 30538, A
37	32	78.0	457	4	US-08-311-731A-52	Sequence 52, Appli
38	32	78.0	488	4	US-08-311-731A-283	Sequence 283, App
39	32	78.0	515	4	US-09-252-991A-28127	Sequence 28127, A
40	32	78.0	548	4	US-09-270-767-45137	Sequence 45137, A
41	32	78.0	574	4	US-09-644-827B-6	Sequence 6, Appli
42	32	78.0	629	4	US-09-270-767-58607	Sequence 58607, A
43	32	78.0	701	4	US-09-270-767-43265	Sequence 43265, A
44	32	78.0	938	4	US-09-637-145-2	Sequence 2, Appli
45	32	78.0	1041	4	US-09-644-827B-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

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US-08-058-699-10
; Sequence 10, Application US/08058699
; Patent No. 5443827
; GENERAL INFORMATION:
; APPLICANT: Edgar Haber
; APPLICANT: Christoph Bode
; APPLICANT: Marschall S. Runge
; TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
; TITLE OF INVENTION: THROMBIN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/058,699
; FILING DATE: 19930503
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser, Ph.D.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: Linear
; US-08-058-699-10

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Query Match 100.0%; Score 41; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 1 GHRPLDK 7

RESULT 2
US-08-058-699-11
; Sequence 11, Application US/08058699
; Patent No. 5443827
; GENERAL INFORMATION:
; APPLICANT: Edgar Haber
; APPLICANT: Christoph Bode
; APPLICANT: Marschall S. Runge
; TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
; TITLE OF INVENTION: THROMBIN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/058,699
; FILING DATE: 19930503
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser, Ph.D.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; STRANDEDNESS: Linear
; TOPOLOGY: Linear
; US-08-058-699-11

Query Match 100.0%; Score 41; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 1 GHRPLDK 7

RESULT 3
US-08-448-547-1
; Sequence 1, Application US/08448547
; Patent No. 5821068
; GENERAL INFORMATION:
; APPLICANT: Soe, Gilbu
; APPLICANT: Kohno, Isao
; APPLICANT: Inuzuka, Kimiko
; APPLICANT: Ito, Yumiko
; TITLE OF INVENTION: ANTI-HUMAN SOLUBLE FIBRIN ANTIBODY,
; TITLE OF INVENTION: HYBRIDOMA, AND IMMUNOASSAYING METHOD
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,547
; FILING DATE: 30-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01844
; FILING DATE: 01-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-297325
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: Q-38931
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-547-1

Query Match 100.0%; Score 41; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 1 GHRPLDK 7

RESULT 4
US-10-142-935-6
; Sequence 6, Application US/10142935
; Patent No. 6835378
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-10-142-935-6

Query Match 100.0%; Score 41; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |

Db 10 GHRPLDK 16

RESULT 5

US-10-142-935-4

; Sequence 4, Application US/10142935

; Patent No. 6835378

; GENERAL INFORMATION:

; APPLICANT: DAVIS, Stacey

; APPLICANT: HOOK, Magnus A.O.

; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION

; FILE REFERENCE: P07201US01/BAS

; CURRENT FILING DATE: 2002-05-13

; PRIOR FILING DATE: 2002-05-13

; PRIOR FILING DATE: 2001-05-13

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 25

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-10-142-935-4

Query Match 100.0%; Score 41; DB 4; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.09;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

Db 15 GHRPLDK 21

RESULT 6

US-08-486-135-12

; Sequence 12, Application US/08486135

; Patent No. 5720934

; GENERAL INFORMATION:

; APPLICANT: Dean, Richard T

; APPLICANT: Buttram, Scott

; APPLICANT: McBride, William

; APPLICANT: Lister-James, John

; APPLICANT: Civitello, Edgar R

; TITLE OF INVENTION: Technetium-99m Labeled Peptides for

; TITLE OF INVENTION: Imaging

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner & Allegretti, Ltd.

; STREET: 10 South Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/486,135

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: No. 5720934nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,205-N

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-470-152-12

Query Match 100.0%; Score 41; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

Db 1 GHRPLDK 7

RESULT 7

US-08-470-152-12

; Sequence 12, Application US/08470152

; Patent No. 5780007

; GENERAL INFORMATION:

; APPLICANT: Dean, Richard T

; APPLICANT: Buttram, Scott

; APPLICANT: McBride, William

; APPLICANT: Lister-James, John

; APPLICANT: Civitello, Edgar R

; TITLE OF INVENTION: Technetium-99m Labeled Peptides for

; TITLE OF INVENTION: Imaging

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner & Allegretti, Ltd.

; STREET: 10 South Wacker Drive, Suite 3000

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/470,152

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: No. 5780007nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,205-L

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-470-152-12

Query Match 100.0%; Score 41; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

Db 1 GHRPLDK 7

RESULT 8

US-08-468-964B-10

; Sequence 10, Application US/08468964B

; Patent No. 5923303

; GENERAL INFORMATION:

APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
CITY: Londonderry
STATE: NH
COUNTRY: USA
ZIP: 03053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,964B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Mcdaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 111D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEFAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-964B-10

Query Match 100.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDK 7
|||||
Db 1 GHRPLDK 7

RESULT 9
US-07-871-282A-10
Sequence 10, Application US/07871282A
Patent No. 5965107
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
CITY: Londonderry
STATE: NH
COUNTRY: USA
ZIP: 03053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/871,282A
FILING DATE: 20-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Mcdaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEFAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-871-282A-10

Query Match 100.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDK 7
|||||
Db 1 GHRPLDK 7

RESULT 10
US-08-290-853-33
Sequence 33, Application US/08290853
Patent No. 5989519
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Buttram, Scott
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,853
FILING DATE: 11-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5989519nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,112-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1

OTHER INFORMATION: /label= BAT
OTHER INFORMATION: /note= "The amino terminus is linked to a BAT
OTHER INFORMATION: radiolabel binding moiety."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 28
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
amide"
US-08-290-853-33

Query Match 100.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 11
US-08-253-678A-10
Sequence 10, Application US/08253678A
Patent No. 5997844
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
TITLE OF INVENTION: IMAGING
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
CITY: Londonderry
STATE: NH
COUNTRY: USA
ZIP: 03053

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,678A
FILING DATE: 03-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 112
TELEPHONE: (603) 437-8970
TELEFAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-253-678A-10

Query Match 100.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 12
US-08-582-134B-10
Sequence 10, Application US/08582134B
Patent No. 6074627
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
TITLE OF INVENTION: IMAGING
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
CITY: Londonderry
STATE: NH
COUNTRY: USA
ZIP: 03053

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,134B
FILING DATE: 14-MAY-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 112D1
TELEPHONE: (603) 437-8970
TELEFAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-582-134B-10

Query Match 100.0%; Score 41; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 13
US-08-170-299-10
Sequence 10, Application US/08170299
Patent No. 6086849
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: TECHNETIUM-99m Labeled Peptides for
TITLE OF INVENTION: IMAGING
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL

;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; FILING DATE: 09-FEB-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 6086849nan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 92,205-H
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-170-299-10

Query Match 100.0%; Score 41; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||
Db 1 GHRPLDK 7

RESULT 14
US-08-290-853-35
; Sequence 35, Application US/08290853
; Patent No. 5985519
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging Inflammation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,853
; FILING DATE: 11-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5985519nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,112-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids

;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1..3
;; OTHER INFORMATION: /label= Picolinoyl
;; OTHER INFORMATION: /note= "The amino terminal residue is
;; OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine is
;; OTHER INFORMATION: protected by an acetamidomethyl group."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 30
;; OTHER INFORMATION: /label= Amide
;; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
;; OTHER INFORMATION: amide"
US-08-290-853-35

Query Match 100.0%; Score 41; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||
Db 3 GHRPLDK 9

RESULT 15
US-08-472-535-9
; Sequence 9, Application US/08472535
; Patent No. 5711931
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lees, Robert S.
; APPLICANT: Buttram, Scott
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging Inflammation
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,535
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5711931nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,112-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= Picolinoyl
; OTHER INFORMATION: /note= "The amino terminal residue is

OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine
residue is protected by an acetoamidomethyl

US-08-472-535-9

Query Match 100.0%; Score 41; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
DB 4 GHRPLDK 10

RESULT 16

US-08-484-774-9

Sequence 9, Application US/08484774
Patent No. 5807538

GENERAL INFORMATION:

APPLICANT: Dean, Richard T

APPLICANT: Lees, Robert S.

APPLICANT: Buttram, Scott

TITLE OF INVENTION: Technetium-99m Labeled Peptides for

TITLE OF INVENTION: Imaging Inflammation

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,774

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: No. 5807538nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,112-K

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1..3

OTHER INFORMATION: /label= Picolinoyl

OTHER INFORMATION: /note= "The amino terminal residue is

pyridine-2-carbonyl; the thiol of the cysteine

residue is protected by an acetoamidomethyl

US-08-484-774-9

Query Match 100.0%; Score 41; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
DB 4 GHRPLDK 10

RESULT 17

US-08-266-178A-9

Sequence 9, Application US/08266178A

Patent No. 6017510

GENERAL INFORMATION:

APPLICANT: Dean, Richard T

APPLICANT: Buttram, Scott

TITLE OF INVENTION: Technetium-99m Labeled Peptides for

TITLE OF INVENTION: Imaging Inflammation

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/266,178A

FILING DATE: 27-JUN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 6017510nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,112

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1..3

OTHER INFORMATION: /label= Picolinoyl

OTHER INFORMATION: /note= "The amino terminal residue is

pyridine-2-carbonyl; the thiol of the cysteine

residue is protected by an acetoamidomethyl

US-08-266-178A-9

Query Match 100.0%; Score 41; DB 3; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
DB 4 GHRPLDK 10

RESULT 18

US-09-513-999C-4232

Sequence 4232, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm
; SEQ ID NO 4232
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -30..-1
; OTHER INFORMATION: score 12.2
; OTHER INFORMATION: seq LLLLLLCVFLVKV/QG
US-09-513-999C-4232

Query Match 100.0%; Score 41; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 19
US-09-513-999C-4231
; Sequence 4231, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4231
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -30..-1
; OTHER INFORMATION: score 12.2
; OTHER INFORMATION: seq LLLLLLCVFLVKV/QG
US-09-513-999C-4231

Query Match 100.0%; Score 41; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 20
US-09-919-039-33
; Sequence 33, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 33

; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 3393861CD1
US-09-919-039-33

Query Match 100.0%; Score 41; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 42 GHRPLDK 48

RESULT 21
US-08-206-176-4
; Sequence 4, Application US/08206176
; Patent No. 5639940
; GENERAL INFORMATION:
; APPLICANT: Garner, Ian
; APPLICANT: Dairymple, Michael A
; APPLICANT: Prunkard, Donna E
; APPLICANT: Foster, Donald C
; TITLE OF INVENTION: Production of Fibrinogen in Transgenic
; TITLE OF INVENTION: Animals
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,176
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-648
; REFERENCE/DOCKET NUMBER: 93-15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-206-176-4

Query Match 100.0%; Score 41; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 22
US-09-949-016-9617
; Sequence 9617, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9617
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9617

Query Match 100.0%; Score 41; DB 4; Length 493;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 47 GHRPLDK 53

RESULT 23
US-10-142-935-9

; Sequence 9, Application US/10142935
; Patent No. 6835378

; GENERAL INFORMATION:

; APPLICANT: DAVIS, Stacey

; APPLICANT: HOOK, Magnus A.O.

; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION

; FILE REFERENCE: P07201US01/BAS

; CURRENT APPLICATION NUMBER: US/10/142,935

; PRIOR FILING DATE: 2002-05-13

; PRIOR APPLICATION NUMBER: US 60/290,072

; PRIOR FILING DATE: 2001-05-13

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-10-142-935-9

Query Match 87.8%; Score 36; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 5 GHRPLD 10

RESULT 24

US-10-142-935-8

; Sequence 8, Application US/10142935

; Patent No. 6835378

; GENERAL INFORMATION:

; APPLICANT: DAVIS, Stacey

; APPLICANT: HOOK, Magnus A.O.

; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION

; FILE REFERENCE: P07201US01/BAS

; CURRENT APPLICATION NUMBER: US/10/142,935

; CURRENT FILING DATE: 2002-05-13

; PRIOR APPLICATION NUMBER: US 60/290,072

; PRIOR FILING DATE: 2001-05-13

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-8

Query Match 87.8%; Score 36; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 10 GHRPLD 15

RESULT 25

US-10-142-935-5

; Sequence 5, Application US/10142935

; Patent No. 6835378

; GENERAL INFORMATION:

; APPLICANT: DAVIS, Stacey

; APPLICANT: HOOK, Magnus A.O.

; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION

; FILE REFERENCE: P07201US01/BAS

; CURRENT APPLICATION NUMBER: US/10/142,935

; CURRENT FILING DATE: 2002-05-13

; PRIOR APPLICATION NUMBER: US 60/290,072

; PRIOR FILING DATE: 2001-05-13

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-10-142-935-5

Query Match 87.8%; Score 36; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 15 GHRPLD 20

RESULT 26

US-09-248-796A-26425

; Sequence 26425, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstein et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 26425

; LENGTH: 74

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-26425

Query Match 87.8%; Score 36; DB 4; Length 74;
Best Local Similarity 85.7%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 68 GHRPADK 74

RESULT 27

US-09-252-991A-23750
; Sequence 23750, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23750
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23750

Query Match 87.8%; Score 36; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 134 GHRPLD 139

RESULT 28

US-09-799-875-5
; Sequence 5, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-875-5

Query Match 85.4%; Score 35; DB 4; Length 1203;
Best Local Similarity 85.7%; Pred. No. 92;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 799 GHRPLSK 805

RESULT 29

US-09-252-991A-28544
; Sequence 28544, Application US/09252991A

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28544
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28544

Query Match 82.9%; Score 34; DB 4; Length 788;
Best Local Similarity 71.4%; Pred. No. 94;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 619 GHRPLER 625

RESULT 30

US-09-252-991A-25874
; Sequence 25874, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25874
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25874

Query Match 80.5%; Score 33; DB 4; Length 305;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 261 GHQPLDQ 267

RESULT 31

US-09-252-991A-26924
; Sequence 26924, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26924
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26924

Query Match 80.5%; Score 33; DB 4; Length 379;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
||| |
Db 85 GHRPADR 91

RESULT 32

US-09-252-991A-22575
; Sequence 22575, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22575

; LENGTH: 497
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22575

Query Match 80.5%; Score 33; DB 4; Length 497;
Best Local Similarity 71.4%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
||| |
Db 40 GHRPMQK 46

RESULT 33

US-09-252-991A-30324
; Sequence 30324, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30324

; LENGTH: 579
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30324

Query Match 80.5%; Score 33; DB 4; Length 579;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
||| |
Db 36 GHRPADR 42

RESULT 34

US-09-252-991A-24235
; Sequence 24235, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24235

; LENGTH: 632
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24235

Query Match 80.5%; Score 33; DB 4; Length 632;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
||| |
Db 243 GHRPLEQ 249

RESULT 35

US-09-252-991A-28870
; Sequence 28870, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28870

; LENGTH: 1020
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28870

Query Match 80.5%; Score 33; DB 4; Length 1020;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
||| |
Db 323 GHRPLDR 329

RESULT 36

US-09-252-991A-30538
; Sequence 30538, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30538
LENGTH: 266
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30538

Query Match 78.0%; Score 32; DB 4; Length 266;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
|||||
Db 189 HRPLDR 194

RESULT 37
US-08-311-731A-52
Sequence 52, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411

CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441

INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-52

Query Match 78.0%; Score 32; DB 4; Length 457;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
|||||
Db 246 GHRPIER 252

RESULT 38
US-08-311-731A-283
Sequence 283, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 283:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Mycobacterium leprae
US-08-311-731A-283

Query Match 78.0%; Score 32; DB 4; Length 488;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 283 GHRPIER 289

RESULT 39
US-09-252-991A-28127
Sequence 28127, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788

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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28127
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28127

Query Match      78.0%; Score 32; DB 4; Length 515;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 HRPLDK 7
Db      408 HRPDR 413

RESULT 40
US-09-270-767-45137
; Sequence 45137, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45137
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45137

Query Match      78.0%; Score 32; DB 4; Length 548;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GHRPLD 6
Db      282 GHRPLE 287

Search completed: June 1, 2005, 11:53:56
Job time : 29 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 11:37:44 ; Search time 112.467 Seconds
(without alignments)
24.072 Million cell updates/sec

Title: US-09-424-940A-1

Perfect score: 41

Sequence: 1 GHRPLDK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	7	1 AAP71314	Aap71314 Sequence
2	41	100.0	7	2 AAR05558	Aar05558 Peptide a
3	41	100.0	7	2 AAR65792	Aar65792 Fibrin-sp
4	41	100.0	7	2 AAR63269	Aar63269 Beta-pept
5	41	100.0	8	1 AAR92686	Aar92686 Human fib
6	41	100.0	8	2 AAR44837	Aar44837 Human fib
7	41	100.0	8	2 AAR65793	Aar65793 Fibrin-sp
8	41	100.0	8	2 AAR63270	Aar63270 Synthetic
9	41	100.0	9	4 ABB76979	Abb76979 Residues
10	41	100.0	10	2 AAW11931	Aaw11931 Fibrinoge
11	41	100.0	12	7 ADD32229	Add32229 Biotinyla
12	41	100.0	12	2 AAR28629	Aar28629 N-termina
13	41	100.0	12	2 AAR44829	Aar44829 Human fib
14	41	100.0	12	2 AAR44838	Aar44838 Human fib
15	41	100.0	14	5 ABB78036	Abb78036 Peptide W
16	41	100.0	16	2 AAR44830	Aar44830 Human fib
17	41	100.0	20	6 AAE34816	Aae34816 S. epider
18	41	100.0	25	6 AAE34814	Aae34814 S. epider
19	41	100.0	28	2 AAR40010	Aar40010 Scintigra
20	41	100.0	28	2 ADD12888	Add12888 scintigra
21	41	100.0	28	5 AAO18333	Aao18333 Fibrinoge
22	41	100.0	29	2 AAR42547	Aar42547 Leukocyte
23	41	100.0	30	2 AAR42546	Aar42546 Leukocyte
24	41	100.0	30	6 ABP56240	Abp56240 Targeting
25	41	100.0	30	8 ADE64331	Ade64331 Radiophar

26	41	100.0	30	8 ADH58575	Adh58575 Radiophar
27	41	100.0	87	4 ABB11339	Abb11339 Human bet
28	41	100.0	118	3 AAG00151	Aag00151 Human sec
29	41	100.0	140	4 AAU33273	Aau33273 Novel hum
30	41	100.0	141	4 AAO10778	Aao10778 Human pol
31	41	100.0	150	3 AAG00150	Aag00150 Human sec
32	41	100.0	453	4 AAM78493	Aam78493 Human pro
33	41	100.0	455	8 ABM85149	Abm85149 Human dia
34	41	100.0	455	8 ABM85150	Abm85150 Human dia
35	41	100.0	474	8 ABM85152	Abm85152 Human dia
36	41	100.0	474	8 ABM84478	Abm84478 Human dia
37	41	100.0	474	8 ABM84481	Abm84481 Human dia
38	41	100.0	474	8 ABM84482	Abm84482 Human dia
39	41	100.0	474	8 ABM85151	Abm85151 Human dia
40	41	100.0	488	8 ADE76868	Ade76868 Human pro
41	41	100.0	491	2 AAR82243	Aar82243 Human fib
42	41	100.0	491	4 AAM78492	Aam78492 Human pro
43	41	100.0	491	6 AAE36413	Aae36413 Human FBG
44	41	100.0	491	7 ADD69271	Add69271 Human fib
45	41	100.0	491	7 ADD69272	Add69272 Human fib

ALIGNMENTS

RESULT 1

AAP71314
ID AAP71314 standard; peptide; 7 AA.

XX
AC AAP71314;
DT 25-MAR-2003 (revised)
DT 03-OCT-2002 (revised)
DT 19-JUN-1991 (first entry)
XX
Sequence of fibrin immunogen for the prepn. of monoclonal antibodies (MABs).
DE
XX Fibrin-specific monoclonal antibody; screening.
OS Homo sapiens.
XX
Key Location/Qualifiers
FT Misc-difference 7 /label= Lys-OH
FT
XX WO8706263-A.
XX
PD 22-OCT-1987.
XX
PF 14-APR-1987; 87WO-US000862.
XX
PR 14-APR-1986; 86US-00851514.
XX
PA (GHEO) GEN HOSPITAL CORP.
PA (GHEO) GEN HOSPITAL CORP.
PA (GHEO) GEN HOSPITAL CORP.
XX
PI Matsueda GR, Haber E;
XX WPI; 1987-306855/43.
XX
PT Screening of fibrin-specific monoclonal antibodies - by contact with immobilised crosslinked fibrin clot and screening with detectable labelling step.
XX
PS Disclosure; Page 7; 41pp; English.
XX
CC The MABs are specific to fibrin without fibrinogen cross-reactivity. They have increased binding to fibrin and in vivo thrombi. The MABs can be used in immunoassays for fibrin in the presence of fibrinogen or other proteins. They can be used as immunoaffinity ligands for the purification of fibrin. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on

```
CC 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 7 AA;
    Query Match      100.0%; Score 41; DB 1; Length 7;
    Best Local Similarity 100.0%; Pred. No. 1.8e+06;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
    |||||
Db 1 GHRPLDK 7

RESULT 2
AAR05558
ID AAR05558 standard; peptide; 7 AA.
XX
AC AAR05558;
XX
DT 25-MAR-2003 (revised)
DT 11-OCT-1990 (first entry)
XX
DE Peptide antigenic to fibrin.
XX
KW fibrin; fibrinogen; thrombi; immunoaffinity.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /label= His or Pro
FT Misc-difference 4 /label= Pro or Val
FT Misc-difference 5 /label= Leu or Val
FT Misc-difference 6 /label= Asp or Glu
FT Misc-difference 7 /label= Lys or Arg
XX
XX US4927916-A.
XX
XX 22-MAY-1990.
XX
XX 30-JAN-1986; 86US-00824228.
XX
XX 23-APR-1984; 84US-00603155.
XX
XX (GHEO ) GEN HOSPITAL CORP.
XX
XX Matsueda BR, Haber E, Hui K;
XX WPI; 1990-185723/24.
XX
XX Fibrin-specific monoclonal antibodies - lacking fibrinogen cross-
XX reactivity, obtd. using peptide(s) comprising fibrin-specific epitopic
XX sequences.
XX
XX Claim 1; Page 17; 12pp; English.
XX
XX Peptide is epitopic to fibrin, allowing anti-fibrin Abs to be raised
XX without cross-reactivity to fibrinogen. They are particularly useful in
XX detection of fibrin and thrombi. (Updated on 25-MAR-2003 to correct PA
XX field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 7 AA;
    Query Match      100.0%; Score 41; DB 2; Length 7;
    Best Local Similarity 100.0%; Pred. No. 1.8e+06;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
    |||||
Db 1 GHRPLDK 7

RESULT 3
AAR65792
ID AAR65792 standard; peptide; 7 AA.
XX
AC AAR65792;
XX
DT 25-MAR-2003 (revised)
DT 26-JUN-1995 (first entry)
XX
DE Fibrin-specific epitopic peptide.
XX
KW Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;
KW antifibrin-specific monoclonal antibodies.
XX
OS Synthetic.
XX
XX US5357042-A.
XX
XX 18-OCT-1994.
XX
XX 24-AUG-1992; 92US-00932729.
XX
XX 23-APR-1984; 84US-00603155.
XX
XX 30-JAN-1986; 86US-00824228.
XX
XX 22-DEC-1989; 89US-00454954.
XX
XX (GHEO ) GEN HOSPITAL CORP.
XX
XX Hui K, Matsueda GR, Haber E;
XX WPI; 1994-332411/41.
XX
XX Synthetic epitopic peptide(s) of variable length - capable of eliciting
XX fibrin specific antibodies free of fibrinogen cross-reactivity.
XX
XX Claim 2; Col 18; 12pp; English.
XX
XX AAR65789-R65794 are synthetic peptides comprising fibrin-specific
XX epitopic sequences, they can be used to prepare hybridoma cell lines,
XX which produce antifibrin-specific monoclonal antibodies substantially
XX devoid of fibrinogen cross-reactivity. These antibodies are useful in the
XX in vivo and in vitro detection of thrombi and fibrin deposits. (Updated
XX on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 7 AA;
    Query Match      100.0%; Score 41; DB 2; Length 7;
    Best Local Similarity 100.0%; Pred. No. 1.8e+06;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
    |||||
Db 1 GHRPLDK 7

RESULT 4
AAR63269
ID AAR63269 standard; peptide; 7 AA.
XX
AC AAR63269;
XX
DT 25-MAR-2003 (revised)
DT 21-JUL-1995 (first entry)
XX
DE Beta-peptide used to raise monoclonal antibody 59D8.
XX
KW Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79;
KW coronary stent implantation; adjunctive therapy; fibrinogen; haemorrhage.
XX
```


OS Synthetic.
 XX WO9425491-A1.
 XX 10-NOV-1994.
 PD
 XX 03-MAY-1994; 94WO-US004881.
 XX
 PF
 XX 03-MAY-1993; 93US-00058699.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA (UYEM-) UNIV EMORY.
 XX
 XX Haber E, Bode C, Runge M;
 PI WPI; 1994-358195/44.
 XX
 DR Fibrin-binding antibody linked to thrombin inhibitor - useful for
 XX preventing blood coagulation by specifically targeting inhibitor to site
 PT of thrombin activity.
 PT
 XX Example 1; Page 13; 53pp; English.
 PS
 XX This sequence represents beta-peptide which was used to raise the
 CC monoclonal antibody 59D8. The antibody binds fibrin and may be used in
 CC the chimeric molecule of the invention. The chimeric molecule further
 CC comprises a thrombin inhibitor linked to the fibrin-binding antibody
 CC through a covalent linkage. The chimeric molecule allows fibrin-specific
 CC antibody targeting of hirudin and other thrombin inhibitors, which is
 CC more potent than thrombin on its own. The epitope to which 59D8 binds
 CC becomes available only after thrombin cleaves fibrinopeptide B. The
 CC chimeric protein may be used for preventing coagulation of the blood.
 CC Anti-thrombin targeting can be esp. useful in highly thrombogenic
 CC situations such as coronary stent implantation and can be used as an
 CC adjunctive therapy with highly selective thrombolytic agents. The
 CC thrombin inhibitor is localised to sites of thrombin activity by the
 CC antibody which binds to thrombin but does not cross react with uncleaved
 CC fibrinogen. The selectivity of inhibition allows the total amount of
 CC thrombin inhibitor used to be substantially reduced, resulting in a
 CC reduced potential for generalised haemorrhaging. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 41; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db |||||
 1 GHRPLDK 7
 RESULT 5
 AAP82686
 ID AAP82686 standard; peptide; 8 AA..
 XX
 AC AAP82686;
 XX
 XX 25-MAR-2003 (revised)
 DT 05-DEC-1990 (first entry)
 XX
 XX Human fibrin beta chain N-terminal.
 DE
 XX Fibrin; beta chain; N-terminal; monoclonal antibody; thrombosis.
 KW
 XX Synthetic.
 OS
 XX JP63093800-A.
 PN
 XX 25-APR-1988.
 PD
 XX 08-OCT-1986; 86JP-00237876.
 PF
 XX 08-OCT-1986; 86JP-00237876.
 XX
 XX (MITN) MITSUBISHI GAS CHEM CO INC.
 PA
 XX WPI; 1988-152086/22.
 DR
 XX New anti-human fibrin mono-clonal antibody, for diagnosing thrombosis -
 PT prepd. from hybridoma obtd. by applying cell fusion mouse spleen and
 PT mouse myeloma-cells, and measures human fibrin.
 XX
 XX Claim 1; Page 1; 8pp; Japanese.
 PS
 XX The peptide is linked to a carrier protein via a linking agent and used
 CC to immunise mice. The mouse spleen cells and amyeloma cell line can be
 CC fused to produce a hybridoma secreting MABs which bind specifically to
 CC human fibrin but not fibrinogen. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 41; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db |||||
 1 GHRPLDK 7
 RESULT 6
 AAR44837
 ID AAR44837 standard; peptide; 8 AA.
 XX
 AC AAR44837;
 XX
 DT 20-JUN-1994 (first entry)
 XX
 DE Human fibrin beta-chain N-terminal peptide A.
 XX
 KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin;
 KW monoclonal antibody; hybridoma; thrombolysis antithrombotic agent;
 KW bispecific antibody.
 XX
 OS Synthetic.
 OS
 XX JP05304992-A.
 PN
 XX 19-NOV-1993.
 PD
 XX 17-JUN-1992; 92JP-00158301.
 PF
 XX 20-JUN-1991; 91JP-00148936.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX WPI; 1993-408334/51.
 DR
 XX Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug
 PT increased thrombolytic activity and specificity and reduced reactivity to
 PT fibrinogen.
 PT
 XX Example 1; Page 14; 38pp; Japanese.
 PS
 XX Human fibrin beta-chain peptides A and B were synthesised and coupled to
 CC BSA for injection into mice. The peptides were used to raise antibodies
 CC to human fibrin. Monoclonal antibodies specific for fibrin are used in
 CC the production of bispecific monoclonal antibodies which also recognise
 CC truncated tPA mutants lacking the finger, EGF and Kringle 1 domains
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 41; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db |||||
 1 GHRPLDK 7
 RESULT 6
 AAP82686
 ID AAP82686 standard; peptide; 8 AA..
 XX
 AC AAP82686;
 XX
 XX 25-MAR-2003 (revised)
 DT 05-DEC-1990 (first entry)
 XX
 XX Human fibrin beta chain N-terminal.
 DE
 XX Fibrin; beta chain; N-terminal; monoclonal antibody; thrombosis.
 KW
 XX Synthetic.
 OS
 XX JP63093800-A.
 PN
 XX 25-APR-1988.
 PD
 XX 08-OCT-1986; 86JP-00237876.
 PF

Best Local Similarity 100.0%; Pred. NO. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 DB 1 GHRPLDK 7

RESULT 7
 AAR65793
 ID AAR65793 standard; peptide; 8 AA.
 AC AAR65793;
 XX
 XX 25-MAR-2003 (revised)
 DT 26-JUN-1995 (first entry)
 XX
 XX Fibrin-specific epitopic peptide.
 DE
 XX Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;
 KW antifibrin-specific monoclonal antibodies.
 XX
 XX Synthetic.
 OS
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 8
 FT /note= "May be absent and if present may be bonded to
 FT keyhole limpet hemocyanin."
 XX
 XX US5357042-A.
 XX
 XX 18-OCT-1994.
 XX
 XX 24-AUG-1992; 92US-00932729.
 XX
 XX 23-APR-1984; 84US-00603155.
 PR 30-JAN-1986; 86US-00824228.
 XX 22-DEC-1989; 89US-00454954.
 XX
 XX (GEO) GEN HOSPITAL CORP.
 PA
 XX Hui X, Matsueda GR, Haber E;
 PI
 XX WPI; 1994-332411/41.
 DR
 XX Synthetic epitopic peptide(s) of variable length - capable of eliciting
 PT fibrin specific antibodies free of fibrinogen cross-reactivity.
 XX
 XX Claim 3; Col 18; 12pp; English.
 PS
 XX AAR65789-R65794 are synthetic peptides comprising fibrin-specific
 CC epitopic sequences, they can be used to prepare hybridoma cell lines,
 CC which produce antifibrin-specific monoclonal antibodies substantially
 CC devoid of fibrinogen cross-reactivity. These antibodies are useful in the
 CC in vivo and in vitro detection of thrombi and fibrin deposits. (Updated
 CC on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 8 AA;
 SQ

Query Match 100.0%; Score 41; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. NO. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 DB 1 GHRPLDK 7

RESULT 8
 AAR63270
 ID AAR63270 standard; peptide; 8 AA.
 XX
 AC AAR63270;

XX
 DT 25-MAR-2003 (revised)
 DT 21-JUL-1995 (first entry)
 XX
 XX Synthetic beta-peptide used to raise monoclonal antibody 59D8.
 DE
 XX Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
 KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; p79;
 KW coronary stent implantation; adjunctive therapy; fibrinogen; haemorrhage.
 XX
 XX Synthetic.
 OS
 XX WO9425491-A1.
 PN
 XX 10-NOV-1994.
 PD
 XX 03-MAY-1994; 94WO-US004881.
 PF
 XX 03-MAY-1993; 93US-00058699.
 PR
 XX (HARD) HARVARD COLLEGE.
 XX (UYEM-) UNIV EMORY.
 PA
 XX
 XX PI Haber E, Bode C, Runge M;
 PI
 XX WPI; 1994-358195/44.
 DR
 XX Fibrin-binding antibody linked to thrombin inhibitor - useful for
 PT preventing blood coagulation by specifically targetting inhibitor to site
 PT of thrombin activity.
 PT
 XX
 PS Example 1; Page 14; 53pp; English.
 XX
 XX This sequence represents a synthetic beta-peptide which was used to
 CC immunopurify the monoclonal antibody 59D8 which was raised against beta-
 CC peptide (see also AAR63269). The antibody binds fibrin and may be used in
 CC the chimeric molecule of the invention. The chimeric molecule further
 CC comprises a thrombin inhibitor linked to the fibrin-binding antibody
 CC through a covalent linkage. The chimeric molecule allows fibrin-specific
 CC antibody targetting of hirudin and other thrombin inhibitors, which is
 CC more potent than thrombin on its own. The epitope to which 59D8 binds
 CC becomes available only after thrombin cleaves fibrinopeptide B. The
 CC chimeric protein may be used for preventing coagulation of the blood.
 CC Anti-thrombin targetting can be esp. useful in highly thrombogenic
 CC situations such as coronary stent implantation and can be used as an
 CC adjunctive therapy with highly selective thrombolytic agents. The
 CC thrombin inhibitor is localised to sites of thrombin activity by the
 CC antibody which binds to thrombin but does not cross react with uncleaved
 CC fibrinogen. The selectivity of inhibition allows the total amount of
 CC thrombin inhibitor used to be substantially reduced, resulting in a
 CC reduced potential for generalised haemorrhaging. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX
 XX Sequence 8 AA;
 SQ

Query Match 100.0%; Score 41; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. NO. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 DB 1 GHRPLDK 7

RESULT 9
 ABB76979
 ID ABB76979 standard; peptide; 9 AA.
 XX
 XX ABB76979;
 AC
 XX 22-JUL-2002 (first entry)
 DT
 XX Residues 45-54 of human fibrinogen beta chain precursor.
 DE

XX KW Anti-arthritis; anti-inflammatory; fibrin; rheumatoid polyarthritis;
 XX KW human; fibrinogen beta chain.
 XX OS Homo sapiens.
 XX PN FR2795735-A1.
 XX PD 05-JAN-2001.
 XX PF 01-JUL-1999; 99FR-00008470.
 XX PR 01-JUL-1999; 99FR-00008470.
 XX PA (UYTO-) UNIV TOULOUSE SABATIER PAUL.
 XX PI Serre G, Sebbag M;
 XX DR WPI; 2001-114394/13.
 XX PT New citrulline-containing polypeptide from fibrin, useful for diagnosis
 XX PT and treatment of rheumatoid polyarthritis.
 XX PS Example 1; Page 12; 23pp; French.
 XX CC The present invention relates to a citrulline (Cit) containing
 XX CC polypeptide derived from all or part of the alpha- or beta-chains of
 XX CC fibrin by substitution of at least one arginine residue by Cit. The Cit
 XX CC containing polypeptides can be used for in vitro diagnosis of rheumatoid
 XX CC polyarthritis (RP), by detecting disease-specific autoantibodies, and
 XX CC therapeutically for neutralising the RP-associated autoimmune response.
 XX CC The present sequence is a fragment (residues 45-54) of the human
 XX CC fibrinogen beta chain precursor, which was used in an example from the
 XX CC invention
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 41; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db |||||
 1 GHRPLDK 7
 RESULT 10
 AAW11931
 ID AAW11931 standard; peptide; 10 AA.
 AC AAW11931;
 XX DT 02-APR-1997 (first entry)
 XX DE Fibrinogen A-alpha-chain residues 17-26.
 XX KW Monoclonal; antibody; human; soluble; fibrin; fibrinogen; urea-treated;
 XX KW des-AAB; A-alpha-chain; immunoassay; diagnosis;
 XX KW disseminated intravascular coagulation.
 XX OS Homo sapiens.
 XX PN WO9512617-A1.
 XX PD 11-MAY-1995.
 XX PF 01-NOV-1994; 94WO-JP001844.
 XX PR 02-NOV-1993; 93JP-00297325.
 XX PA (IATR) IATRON LAB INC.
 XX PI Soe G, Kohno I, Inuzuka K, Ito Y;
 WPI; 1995-206667/27.
 Monoclonal antibody reactive with soluble human fibrin - but not with
 fibrinogen, is useful for fibrin immunoassay in plasma specimens.
 Example 3; Page 15; 32pp; Japanese.
 A novel monoclonal antibody (Mab) reacts with human soluble fibrin, but
 not with human fibrinogen. Specifically when the Mab reacts with urea-
 treated des-AAB fibrin the reaction is not inhibited by peptides
 corresponding to fibrinogen A-alpha-chain residues 17-26 (AAW11931), B-
 beta-chain residues 15-24 (AAW11932) or gamma-chain residues 312-324
 (AAW11933). The Mab is useful in immunoassays for soluble fibrin in
 plasma samples (e.g. by sandwich immunoassay), particularly for the
 diagnosis of pathological conditions such as disseminated intravascular
 coagulation
 XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 41; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db |||||
 1 GHRPLDK 7
 RESULT 11
 ADD32229
 ID ADD32229 standard; peptide; 11 AA.
 XX AC ADD32229;
 XX DT 15-JAN-2004 (first entry)
 XX DE Biotinylated fibrin polymerisation associated control peptide.
 XX KW antirheumatic; antiinflammatory; antiarthritic; peptide therapy;
 XX KW proinflammatory; tetrapeptide; inflammation; synovial joint inflammation;
 XX KW rheumatoid arthritis; fibrinogen A alpha chain; fibrin polymerisation;
 XX KW human.
 XX OS Synthetic.
 XX PN US2003109431-A1.
 XX PD 12-JUN-2003.
 XX PF 17-AUG-2001; 2001US-00931009.
 XX PR 17-AUG-2001; 2001US-00931009.
 XX PA (SMIT/) SMITH T H.
 XX PI Smith TH;
 XX DR WPI; 2003-829401/77.
 XX PT Inducing proinflammatory effects in human synovial or fibroblast cells
 XX PT comprises using a specific tetrapeptide which can also identify a
 XX PT receptor to the tetrapeptide.
 XX PS Disclosure; Page 5; 16pp; English.
 XX CC The invention describes a method of inducing proinflammatory effects in
 XX CC synovial or fibroblast cells comprising exposing the cells to a specific
 XX CC tetrapeptide (GPRP) peptide (I). (I) is used for inducing proinflammatory
 XX CC effects in synovial or fibroblast cells. An analogue of (I) is used for
 XX CC treating or preventing inflammation of a synovial joint or rheumatoid
 XX CC arthritis in a subject. (I) is used to identify a receptor for (I).
 XX CC comprising exposing several fibroblastic cells or synovial cells to (I).

CC (1) Can identify, isolate and clone the cell receptor to which it binds.
 CC This is the amino acid sequence of a control peptide associated with the
 CC inhibition of fibrin polymerisation.

XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 41; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 |||||
 Db 1 GHRPLDK 7

RESULT 12.

AAR28629
 ID AAR28629 standard; peptide; 12 AA.

XX
 AC AAR28629;

XX 25-MAR-2003 (revised)
 DT 22-MAR-1993 (first entry)

DE N-terminal human fibrin peptide.

XX bispecific hybrid monoclonal antibody; thrombolytic agent;
 KW cardiac infarction; arterial embolism; cerebral infarction;
 KW peripheral arterial/venous obstruction; retinal arterial obstruction.
 XX

OS Homo sapiens.

XX EP513778-A2.

XX 19-NOV-1992.

PF 14-MAY-1992; 92EP-00108134.

XX 17-MAY-1991; 91JP-00112874.

PR 13-MAR-1992; 92JP-00055025.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Iwasa S, Kurokawa T, Watanabe A;

PI WPI; 1992-383677/47.

XX Bi:specific antibody useful for treating thrombotic obstructive diseases
 PT e.g. cardiac infarction - comprises antithrombus antibody variable region
 PT and anti-thrombolytic substance antibody variable region with no heavy
 PT chain constant region domains 2 and 3.

XX Disclosure; Page 3; 30pp; English.

XX This sequence represents an N-terminal peptide of human fibrin. It was
 CC used in the production of bispecific monoclonal antibodies which are
 CC specific for fibrins, but do not bind fibrinogen, and are specific
 CC for anti-thrombolytic substance. The compen. contg. these Abs lacks the
 CC side effects of prior art Ab targetted thrombolytic agents and has
 CC enhanced thrombolytic activity. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 12 AA;

Query Match 100.0%; Score 41; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 |||||
 Db 1 GHRPLDK 7

RESULT 13

AAR44829
 ID AAR44829 standard; peptide; 12 AA.

XX
 AC AAR44829;

XX 20-JUN-1994 (first entry)

DE Human fibrin beta-chain N-terminal peptide (1-11)-Cys.

XX Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin;
 KW monoclonal antibody; hybridoma; thrombolysis antithrombotic agent;
 KW bispecific antibody.

XX Synthetic.

XX Location/Qualifiers

Key Region 1..11 /note= "human fibrin beta-chain residues 1-11"

FT Modified-site 12

FT /note= "BSA carrier is attached to Cys"

XX JP05304992-A.

PN 19-NOV-1993.

XX 17-JUN-1992; 92JP-00158301.

XX 20-JUN-1991; 91JP-00148936.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 1993-408334/51.

XX Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug
 PT increased thrombolytic activity and specificity and reduced reactivity to
 PT fibrinogen.

XX Disclosure; Page 9; 38pp; Japanese.

XX Human fibrin beta-chain N-terminal peptide (1-11)-Cys was synthesised and
 CC coupled to BSA for injection into mice. The peptide was used to raise
 CC antibodies to human fibrin. Monoclonal antibodies specific for fibrin are
 CC used in the production of bispecific monoclonal antibodies which also
 CC recognise truncated tPA muteins lacking the finger, EGF and Kringle 1
 CC domains

XX Sequence 12 AA;

Query Match 100.0%; Score 41; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 |||||
 Db 1 GHRPLDK 7

RESULT 14

AAR44838
 ID AAR44838 standard; peptide; 12 AA.

XX
 AC AAR44838;

XX 20-JUN-1994 (first entry)

DE Human fibrin beta-chain peptide B.

XX Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin;
 KW monoclonal antibody; hybridoma; thrombolysis antithrombotic agent;
 KW bispecific antibody.

XX Synthetic.

XX JP05304992-A.
 XX 19-NOV-1993.
 XX
 XX 17-JUN-1992; 92JP-00158301.
 XX
 XX 20-JUN-1991; 91JP-00148936.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX WPI; 1993-408334/51.
 XX
 XX Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug
 PT increased thrombolytic activity and specificity and reduced reactivity to
 PT fibrinogen.
 XX
 XX Example 1; Page 14; 38pp; Japanese.
 XX
 XX Human fibrin beta-chain peptides A and B were synthesised and coupled to
 CC BSA for injection into mice. The peptides were used to raise antibodies
 CC to human fibrin. Monoclonal antibodies specific for fibrin are used in
 CC the production of bispecific monoclonal antibodies which also recognise
 CC truncated tPA muteins lacking the finger, EGF and Kringle 1 domains
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 100.0%; Score 41; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB |||||
 6 GHRPLDK 12
 RESULT 15
 ABB78036
 ID ABB78036 standard; peptide; 14 AA.
 AC
 AC ABB78036;
 XX
 XX 22-OCT-2002 (first entry)
 XX
 XX Peptide WTM250 derived from fibrin/fibrinogen beta chain.
 DE
 XX Fibrin beta chain; fibrinogen beta chain; fibrin fragment E;
 KW cell proliferation; angiogenesis; fibrogenesis; collagen synthesis;
 KW wound healing; skin graft; heart muscle revascularisation;
 KW limb replacement; ischaemia; scarring; restenosis; atherosclerosis;
 KW rheumatoid arthritis; diabetes; renal disease; psoriasis;
 KW macular degeneration; cancer; fibrin glue; stent; angioplasty;
 KW antenapedia protein; membrane translocation.
 XX
 XX Synthetic.
 OS
 XX W0200248181-A1.
 PN
 XX 20-JUN-2002.
 XX
 XX 12-DEC-2001; 2001WO-GB005505.
 PF
 XX 12-DEC-2000; 2000GB-00030309.
 PR
 XX (UYAB-) UNIV ABERDEEN.
 XX
 XX Melvin WT, Thompson WD, Stirk CM;
 PI
 XX WPI; 2002-590565/63.
 DR
 XX Novel peptides acting as modulators of fibrin fragment E activity for
 PT treating disease responding to stimulation or inhibition of cell
 PT proliferation or angiogenesis e.g. wound healing, ischemia, cancer and

PT psoriasis.
 XX
 PS Example 3; Page 46; 84pp; English.
 XX
 CC The specification describes peptides which correspond to portions of
 CC fibrin/fibrinogen beta chain sequences, and act as modulators of fibrin
 CC fragment E activity, and in turn modulators of fibrin E effects. Such
 CC effects include induction of cell proliferation, angiogenesis, and
 CC fibrogenesis and collagen synthesis. The peptides are used for wound
 CC healing, increasing effectiveness of skin grafts, revascularisation of
 CC heart muscle or limb replacement surgery. They are also used for treating
 CC ischaemia, reduction of scarring, and prevention of restenosis. The
 CC peptides may also be used for treating atherosclerosis, rheumatoid
 CC arthritis, diabetes, renal disease, psoriasis, macular degeneration, or
 CC cancer. The peptides are also useful for modifying fibrin glues, and may
 CC be incorporated into a stent which is introduced into the arteries of the
 CC patient during an angioplasty procedure for preventing restenosis.
 CC ABB78036-38 represent peptides derived from fibrin/fibrinogen beta chain
 CC sequences. The peptides are derived from the region where plasmin cleaves
 CC the molecule, and contain a C-terminal Cys which does not appear in the
 CC wild type protein
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 41; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB |||||
 1 GHRPLDK 7
 RESULT 16
 AAR44830
 ID AAR44830 standard; peptide; 16 AA.
 XX
 AC AAR44830;
 XX
 XX 20-JUN-1994 (first entry)
 DT
 XX Human fibrin beta-chain internal peptide fragment.
 DE
 XX Tissue plasminogen activator; t-PA; mutein; fibrin; antigen; anti-fibrin;
 KW monoclonal antibody; hybridoma; thrombolysis antithrombotic agent;
 KW bispecific antibody.
 KW
 XX Synthetic.
 OS
 XX JP05304992-A.
 PN
 XX 19-NOV-1993.
 PD
 XX 17-JUN-1992; 92JP-00158301.
 PF
 XX 20-JUN-1991; 91JP-00148936.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX WPI; 1993-408334/51.
 DR
 XX Hybrid monoclonal antibody - used for prepn. of thrombolytic having drug
 PT increased thrombolytic activity and specificity and reduced reactivity to
 PT fibrinogen.
 XX
 XX Disclosure; Page 9; 38pp; Japanese.
 PS
 XX Human fibrin internal peptide fragment was identified as a candidate
 CC immunogen to raise antibodies to human fibrin. Monoclonal antibodies
 CC specific for fibrin are used in the production of bispecific monoclonal
 CC antibodies which also recognise truncated tPA muteins lacking the finger,
 CC EGF and Kringle 1 domains
 CC
 XX

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SQ Sequence 16 AA;
Query Match      100.0%; Score 41; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 6 GHRPLDK 12

RESULT 17
AAE34816
ID AAE34816 standard; peptide; 20 AA.
XX AC AAE34816;
XX DT 28-MAY-2003 (first entry)
XX DE S. epidermidis fibrinogen (Fg) Bbeta chain peptide, beta6-25.
XX KW Thrombin-induced blood coagulation; myocardial infarction; SdrG protein;
XX KW sickle-cell crisis; venous thrombosis; stroke; therapy; anticoagulant;
XX KW fibrinogen; Fg.
XX OS Staphylococcus epidermidis.
XX PN WO200292117-A1.
XX PD 21-NOV-2002.
XX PF 13-MAY-2002; 2002WO-US014741.
XX PR 11-MAY-2001; 2001US-0290072P.
XX PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX PI Davis S, Hook MAO;
XX DR WPI; 2003-140257/13.
XX CC The invention relates to a method for treating or preventing thrombin-
XX CC induced coagulation of blood by administering a SdrG protein. The method
XX CC is sued for preparing a composition for treating myocardial infarction,
XX CC stroke, sickle-cell crisis or venous thrombosis. The present sequence is
XX CC Staphylococcus epidermidis fibrinogen (Fg) Bbeta chain peptide used to
XX CC illustrate the method of the invention
XX PS Example 1; Col 19; 29pp; English.
XX PI Davis S, Hook MAO;
XX DR WPI; 2003-140257/13.
XX CC Treating or preventing thrombin-induced coagulation of blood for treating
XX CC a disease condition such as stroke, myocardial infarction, sickle-cell
XX CC crisis or venous thrombosis by administering a SdrG protein.
XX PS Example 1; Col 19; 29pp; English.
XX CC The invention relates to a method for treating or preventing thrombin-
XX CC induced coagulation of blood by administering a SdrG protein. The method
XX CC is sued for preparing a composition for treating myocardial infarction,
XX CC stroke, sickle-cell crisis or venous thrombosis. The present sequence is
XX CC Staphylococcus epidermidis fibrinogen (Fg) Bbeta chain peptide used to
XX CC illustrate the method of the invention
XX PS Sequence 25 AA;
Query Match      100.0%; Score 41; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 15 GHRPLDK 21

RESULT 19
AAE40010
ID AAR40010 standard; peptide; 28 AA.
XX AC AAR40010;
XX DT 25-MAR-2003 (revised)
XX DT 23-MAY-1994 (first entry)
XX DE Scintigraph imaging agent specific binding peptide.
XX KW Reagent; site imaging; technetium-99M labelled; peptide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 28
XX FT /note= "C-terminal amide"
XX PN WO9321962-A1.
XX PD 11-NOV-1993.
XX PF 19-APR-1993; 93WO-US003687.
XX PR 20-APR-1992; 92US-00871282.
XX

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PA (DIAT-) DIATECH INC.
 XX Dean RT, Buttram S, McBride W, Lister-James J, Civitello ER;
 XX WPI; 1993-368429/46.
 DR Reagents for preparing scintigraphic imaging agents - contg. technetium-
 PT 99m labelled peptide(s) contg. 3-100 aminoacid(s).
 XX Claim 35; Page 39; 55pp; English.
 XX The sequence is that of a specific binding peptide used as part of a
 CC reagent for preparing a scintigraphic imaging agent for imaging sites
 CC within a mammalian body. In this the peptide is covalently linked to a
 CC radiolabel-binding moiety which is capable of forming a complex with a
 CC radioisotope, pref. technetium-99m. (Updated on 25-MAR-2003 to correct PN
 CC field.) (Updated on 25-MAR-2003 to correct PR field.)
 XX Sequence 28 AA;
 SQ

Query Match 100.0%; Score 41; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 |||||
 Db 1 GHRPLDK 7

RESULT 20
 ADD12888
 ID ADD12888 standard; peptide; 28 AA.
 XX
 AC ADD12888;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE scintigraphic imaging agent associated peptide #12.
 XX
 KW imaging; scintigraphic imaging agent; SIA; Technetium-99m; tumour;
 KW somatostatin receptor; leukocytes; atherosclerotic plaque;
 KW deep vein thrombosis.
 XX
 OS Synthetic.
 XX
 PN WO9533498-A1.
 XX
 PD 14-DEC-1995.
 XX
 PF 01-JUN-1995; 95WO-US007017.
 XX
 PR 03-JUN-1994; 94US-00253678.
 XX
 PA (DIAT-) DIATECH INC.
 XX
 PI Dean RT, Buttram S, McBride W, Lister-James J, Civitello ER;
 XX WPI; 1996-039983/04.
 DR Scintigraphic imaging agent comprising specific binding peptide -
 PT attached via an amino acid side chain to a radio:label binding gp.,
 PT provides rapid imaging of tumours, thrombosis etc.
 XX
 PS Claim 14; Page 34; 43pp; English.
 XX The invention describes a reagent (A) for producing an agent for imaging
 CC sites in a mammal comprising a specific binding peptide (I) of 3-100
 CC amino acids and, covalently linked to the side chain of an amino acid,
 CC residue in (I), a radiolabel binding group (II). Also new are (1)
 CC scintigraphic imaging agents (SIA) containing (A) in which (II) is bound
 CC to a radiolabel; (2) kits for preparation of a radiopharmaceutical
 CC comprising (A) and enough reducing agent to label (A) with Technetium-
 CC 99m. Depending on the nature of (I), SIA can be used to image e.g.

CC tumours that express somatostatin receptors; leukocytes; atherosclerotic
 CC plaque; and deep vein thrombosis. Attachment of (II) to a sidechain
 CC avoids any interference with the specific binding properties of (I) and
 CC makes possible derivatisation of cyclic peptides (which are more
 CC resistant to proteolysis). Images may be recorded only a few minutes
 CC after injection of SIA. This is the amino acid sequence of a peptide
 CC associated with the imaging methods of the invention.
 XX Sequence 28 AA;
 SQ

Query Match 100.0%; Score 41; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 |||||
 Db 1 GHRPLDK 7

RESULT 21
 AA018333
 ID AA018333 standard; peptide; 28 AA.
 XX
 AC AA018333;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE Fibrinogen based therapeutic peptide #9.
 XX
 KW Fibrin; fibrinogen; antagonist; inflammation; autoimmune disease;
 KW rheumatic disease; organ transplantation; arteriosclerosis;
 KW reperfusion trauma; thrombosis; cancer; antiinflammatory; antibacterial;
 KW immunosuppressive; antirheumatic; antiatherosclerotic; vasotropic;
 KW thrombolytic; anticoagulant; cytostatic; antipsoriatic.
 XX
 OS Unidentified.
 XX
 PN WO200248180-A2.
 XX
 PD 20-JUN-2002.
 XX
 PF 07-DEC-2001; 2001WO-AT000387.
 XX
 PR 12-DEC-2000; 2000AT-00002063.
 XX
 PA (FIBR-) FIBREX MEDICAL RES. & DEV GMBH.
 XX
 PI Petzelbauer P;
 XX
 DR WPI; 2002-557605/59.
 XX
 PT Peptides or proteins based on fibrin or fibrinogen sequences, useful for
 PT combating fibrin-mediated disorders such as inflammation, transplant
 PT rejection, arteriosclerosis and reperfusion damage.
 XX
 PS Claim 5; Page 40; 41pp; German.
 XX
 CC The present invention relates to peptides based on the alpha- and beta-
 CC chain sequences of fibrin/fibrinogen, which are capable of acting as
 CC fibrin antagonists. These are used for the therapy of local and
 CC generalised inflammation associated with infection, autoimmune reactions,
 CC rheumatic disease, immune system dysfunction or genetic disease, for the
 CC prevention and treatment of organ transplantation rejection reactions,
 CC arteriosclerosis, reperfusion trauma, thrombotic disease and increased
 CC fibrin deposition associated with aging, or for the transport of other
 CC medicaments to human or animal endothelial cells. They may also be
 CC effective against fibrin-mediated tumour growth, collagenosis or
 CC psoriasis. The present sequence is a peptide of the invention
 XX Sequence 28 AA;
 SQ

Query Match 100.0%; Score 41; DB 5; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.097;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 | | | | |
 Db 1 GHRPLDK 7

RESULT 22
 AAR42547
 ID AAR42547 standard; peptide; 29 AA.
 XX AC AAR42547;
 XX DT 25-MAR-2003 (revised)
 XX DT 05-AUG-1994 (first entry)
 XX DE Leukocyte-binding peptide which can bind to technetium-99m.
 XX KW Leukocyte binding peptide; fibrinopeptide B chain; scintigraphic imaging;
 XX KW inflammation site; technetium 99m.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Modified-site 1 /label= OTHER
 XX FT /note= "BAT, i.e. N6,N9-bis(2-methyl- 2-mercaptopropyl) -
 6,9-diazananoic acid"
 XX FT Modified-site 29
 XX FT /note= "Arg-NH2"
 XX PN WO9317719-A1.
 XX PD 16-SEP-1993.
 XX PF 12-MAR-1993; 93WO-US002320.
 XX PR 13-MAR-1992; 92US-00851074.
 XX PA (DIAT-) DIA TECH INC.
 XX PI Dean RT, Lees RS, Buttram S, Lister-James J;
 XX WPI; 1993-303154/38.
 XX DR WO9317719-A1.
 XX PD 16-SEP-1993.
 XX PF 12-MAR-1993; 93WO-US002320.
 XX PR 13-MAR-1992; 92US-00851074.
 XX PA (DIAT-) DIA TECH INC.
 XX PI Dean RT, Lees RS, Buttram S, Lister-James J;
 XX WPI; 1993-303154/38.
 XX DR Scintigraphic imaging agent for sites of inflammation - comprising
 XX PT leukocyte-binding peptide bound technetium-99m via binding moiety.
 XX PS Claim 15; Page 31; 40pp; English.

New peptides are claimed which are leukocyte binding peptides having covalently bound to them a moiety which can bind a Tc-99m radiolabel. The peptides having Tc-99m bound to them are useful as scintigraphic imaging agents for imaging sites of infection and inflammation in the mammalian body, e.g. caused by ischaemia, inflammatory bowel disorder, arthritis or tumours. The present sequence is a specifically claimed example of such a peptide derived from fibrinopeptide B chain. (Updated on 25-MAR-2003 to correct PN field.)

Query Match 100.0%; Score 41; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 | | | | |
 Db 2 GHRPLDK 8

RESULT 23
 AAR42546
 ID AAR42546 standard; peptide; 30 AA.

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 | | | | |
 Db 2 GHRPLDK 8

RESULT 24
 ABP56240
 ID ABP56240 standard; peptide; 30 AA.
 XX AC ABP56240;
 XX DT 28-MAR-2003 (first entry)
 XX DE Targeting moiety peptide SEQ ID NO:5.
 XX KW Targeting moiety; stabilisation; radiopharmaceutical;
 XX KW hydrophilic thioether; hydrophilic 6-hydroxy-chroman.
 XX OS Synthetic.

XX AAR42546;
 XX AC 25-MAR-2003 (revised)
 XX DT 05-AUG-1994 (first entry)
 XX DE Leukocyte-binding peptide which can bind to technetium-99m.
 XX KW Leukocyte binding peptide; fibrinopeptide B chain; scintigraphic imaging;
 XX KW inflammation site; technetium 99m.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Modified-site 1 /note= "picolinoyl-Gly"
 XX FT Modified-site 2 /note= "acetamidomethyl-Cys"
 XX PN WO9317719-A1.
 XX PD 16-SEP-1993.
 XX PF 12-MAR-1993; 93WO-US002320.
 XX PR 13-MAR-1992; 92US-00851074.
 XX PA (DIAT-) DIA TECH INC.
 XX PI Dean RT, Lees RS, Buttram S, Lister-James J;
 XX WPI; 1993-303154/38.
 XX DR Scintigraphic imaging agent for sites of inflammation - comprising
 XX PT leukocyte-binding peptide bound technetium-99m via binding moiety.
 XX PS Claim 15; Page 31; 40pp; English.

New peptides are claimed which are leukocyte binding peptides having covalently bound to them a moiety which can bind a Tc-99m radiolabel. The peptides having Tc-99m bound to them are useful as scintigraphic imaging agents for imaging sites of infection and inflammation in the mammalian body, e.g. caused by ischaemia, inflammatory bowel disorder, arthritis or tumours. The present sequence is a specifically claimed example of such a peptide derived from fibrinopeptide B chain. (Updated on 25-MAR-2003 to correct PN field.)

Query Match 100.0%; Score 41; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 | | | | |
 Db 3 GHRPLDK 9

RESULT 24
 ABP56240
 ID ABP56240 standard; peptide; 30 AA.
 XX AC ABP56240;
 XX DT 28-MAR-2003 (first entry)
 XX DE Targeting moiety peptide SEQ ID NO:5.
 XX KW Targeting moiety; stabilisation; radiopharmaceutical;
 XX KW hydrophilic thioether; hydrophilic 6-hydroxy-chroman.
 XX OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 30 /note= "amidated"
 FT
 FN WO200260491-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 24-OCT-2001; 2001WO-US050423.
 XX
 XX 24-OCT-2000; 2000US-00694992.
 PR 24-OCT-2000; 2000US-00695360.
 PR 24-OCT-2000; 2000US-00695494.
 XX
 XX (DIAT-) DIATIDE INC.
 XX
 XX Cyr JE, Pearson DA;
 PI WPI; 2003-092782/08.
 XX
 XX Composition useful for increasing shelf life of diagnostic and
 PT therapeutic radiopharmaceuticals, comprising radiopharmaceutical
 PT precursor and hydrophilic thioether and/or hydrophilic 6-hydroxy-chroman
 PT derivative.
 XX
 XX Claim 15; Page 48; 64pp; English.
 PS
 XX The present invention describes a composition (C) comprising a
 CC radiopharmaceutical precursor and a stabiliser selected from hydrophilic
 CC thioether (I) and/or hydrophilic 6-hydroxy-chroman derivative (II). Also
 CC described: (1) stabilising a radiopharmaceutical comprising: combining
 CC the radiopharmaceutical precursor with (I) and/or (II) in a container,
 CC and adding a radionuclide to the container; and (2) a kit comprising a
 CC sealed vial containing the radiopharmaceutical precursor, and (I) and/or
 CC (II). (C) can be used to increase the shelf life of diagnostic and
 CC therapeutic radiopharmaceutical precursors in nuclear medicine. The
 CC stabilisers maintain the radiochemical purity of the radiopharmaceutical
 CC to at least 85, preferably at least 90% of the labeled undegraded
 CC radiopharmaceutical. (C) is suitable for stabilising a wide variety of
 CC radiopharmaceuticals. The present sequence represents a specifically
 CC claimed targeting moiety peptide for a composition from the present
 CC invention
 XX
 SQ Sequence 30 AA;
 Query Match 100.0%; Score 41; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB |||||
 4 GHRPLDK 10
 RESULT 25
 ADE64331
 ID ADE64331 standard; peptide; 30 AA.
 XX
 XX ADE64331;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 XX Radiopharmaceutical composition stabilising hydrophilic thioether #5.
 DE
 XX radiopharmaceutical precursor; hydrophilic thioether;
 KW radiopharmaceutical composition; diagnosis; therapy; shelf life;
 KW diagnostic radiopharmaceutical; therapeutic radiopharmaceutical.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 30 /note= "C-terminal amide"
 FT
 FT
 FN US2003103895-A1.
 XX
 XX 05-JUN-2003.
 PD
 XX 24-APR-2002; 2002US-00131546.
 PF
 XX 24-OCT-2000; 2000US-00695494.
 PR 24-OCT-2001; 2001WO-US050423.
 PR
 XX (CYRJ/) CYR J E.
 PA (PEAR/) PEARSON D A.
 XX
 XX Cyr JE, Pearson DA;
 PI WPI; 2004-040976/04.
 XX
 XX Composition used in diagnosis and therapy comprises stabilizing amount of
 PT hydrophilic thioether and radiopharmaceutical precursor or peptide or
 PT benzodiazepine derivative.
 XX
 XX Claim 13; SEQ ID NO 5; 19pp; English.
 PS
 XX The invention describes a composition comprising a radiopharmaceutical
 CC precursor and a stabilising amount of a hydrophilic thioether. The
 CC composition is useful as stabiliser of radiopharmaceutical compositions
 CC for use in diagnosis and therapy. The composition is particularly useful
 CC for increasing the shelf life of diagnostic or therapeutic
 CC radiopharmaceuticals. This the amino acid sequence of a hydrophilic
 CC thioether used in the method of stabilising radiopharmaceutical
 CC compositions.
 XX
 SQ Sequence 30 AA;
 Query Match 100.0%; Score 41; DB 8; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB |||||
 4 GHRPLDK 10
 RESULT 26
 ADH58575
 ID ADH58575 standard; peptide; 30 AA.
 XX
 XX ADH58575;
 AC
 XX 25-MAR-2004 (first entry)
 DT
 XX Radiopharmaceutical composition stabilising peptide #5.
 DE
 XX radiopharmaceutical precursor; hydrophilic 6-hydroxy-chroman derivative;
 KW stabiliser; radiopharmaceutical composition; diagnosis; therapy;
 KW shelf life.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 29 /note= "C-terminal amide"
 FT
 FT
 FN US2003103895-A1.
 XX
 XX 05-JUN-2003.
 PD
 XX 24-APR-2002; 2002US-00131546.
 PF
 XX 24-OCT-2000; 2000US-00695494.
 PR 24-OCT-2001; 2001WO-US050423.
 PR
 XX (CYRJ/) CYR J E.
 PA

PA (PEAR/) PEARSON D A.
XX
PI Cyr JE, Pearson DA;
XX
XX WPI; 2004-106449/11.
XX
XX Compositions, useful as stabilizers, or for increasing shelf life, of
PT radiopharmaceuticals for use in diagnosis or therapy, comprises
PT radiopharmaceutical precursor, hydrophilic thioether and hydrophilic 6-
XX hydroxy-chroman derivative,.
XX
PS Claim 16; SEQ ID NO 5; 17pp; English.
XX
CC The invention describes a composition comprising a radiopharmaceutical
CC precursor and a hydrophilic 6-hydroxy-chroman derivative. The composition
CC is useful as stabilizers of radiopharmaceutical compositions for use in
CC diagnosis and therapy. The composition is particularly useful for
CC increasing the shelf life of diagnostic or therapeutic
CC radiopharmaceuticals. This is the amino acid sequence of a peptide used
CC in the stabilisation of radiopharmaceutical compositions.
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 41; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 4 GHRPLDK 10

RESULT 27
ABBL1339
ID ABBL1339 standard; peptide; 87 AA.
XX
AC ABBL1339;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human beta-fibrinogen homologue, SEQ ID NO:1709.
XX
XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer.
XX
OS Homo sapiens.
XX
XX WO200157188-A2.
XX
XX 09-AUG-2001.
PD
XX
XX 05-FEB-2001; 2001WO-US003800.
XX
XX 03-FEB-2000; 2000US-00496914.
PR
XX 27-APR-2000; 2000US-00560875.
XX
XX (HYSB-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT;
PI
XX WPI; 2001-457740/49.
DR
XX N-PSDB; ABA08583.

XX
PT Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
XX Claim 20; Page 167; 1963pp; English.
PS
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, and hence
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth factor activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention
XX
SQ Sequence 87 AA;

Query Match 100.0%; Score 41; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 31 GHRPLDK 37

RESULT 28
AAG00151
ID AAG00151 standard; protein; 118 AA.
XX
AC AAG00151;
XX
XX 06-OCT-2000 (first entry)
DT
XX
XX Human secreted protein, SEQ ID NO: 4232.
DE
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW Gene therapy; chromosome mapping.
KW
XX Homo sapiens.
OS
XX
XX EP1033401-A2.
PN
XX

```

PD 06-SEP-2000.
XX
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GEST ) GENSET.
XX
XX Dumas Mine Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX N-PSDB; AAC00157.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 13; SEQ ID NO 4232; 71pp + Sequence Listing; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number of
XX 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX tissues. EST sequences usually correspond mainly to the 3' untranslated
XX region (UTR) of the mRNA because they are often obtained from oligo-dT
XX primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
XX sequences derived from the 5' ends of mRNAs and even in those cases where
XX longer cDNA sequences have been obtained, the full 5' UTR is rarely
XX included. 5' ESTs are derived from mRNAs with intact 5' ends and can
XX therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
XX are also used in diagnostic, forensic, gene therapy and chromosome
XX mapping procedures. They are used to obtain upstream regulatory sequences
XX and to design expression and secretion vectors
XX
XX SQ Sequence 118 AA;
    Query Match 100.0%; Score 41; DB 3; Length 118;
    Best Local Similarity 100.0%; Pred. NO. 0.53;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 45 GHRPLDK 51

RESULT 29
AAU33273
ID AAU33273 standard; protein; 140 AA.
AC AAU33273;
XX
XX 18-DEC-2001 (first entry)
XX
XX Novel human secreted protein #3764.
XX
XX Human; vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200179449-A2.
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US008656.
XX
XX 18-APR-2000; 2000US-00552929.
XX 26-JAN-2001; 2001US-00770160.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX Claim 20; SEQ ID NO 24670; 1399pp + Sequence Listing; English.

DR WPI; 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy.
XX
XX Claim 20; Page 752; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
XX determining the presence of or predisposition to a disease associated
XX with altered levels of polypeptide. The polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them. Cells
XX expressing the proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression or
XX physiological interactions of the polypeptide. Vectors comprising the
XX nucleic acids encoding the polypeptides and cells genetically engineered
XX to express them are also useful for producing the proteins. The proteins
XX are useful in genetic vaccination, testing and therapy, and can be used
XX as nutritional supplements. They may be used to increase stem cell
XX proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
XX and/or nerve tissue growth or regeneration; immune suppression and/or
XX stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX AAU29510-AAU33304 represent the amino acid sequences of novel human
XX secreted proteins of the invention
XX
XX SQ Sequence 140 AA;
    Query Match 100.0%; Score 41; DB 4; Length 140;
    Best Local Similarity 100.0%; Pred. NO. 0.65;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 45 GHRPLDK 51

RESULT 30
AAU10778
ID AAU10778 standard; protein; 141 AA.
XX
XX AAU10778;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 24670.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US004927.
XX
XX 28-FEB-2000; 2000US-00515126.
XX 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-514838/56.
XX N-PSDB; AA190709.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 20; SEQ ID NO 24670; 1399pp + Sequence Listing; English.

```

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 141 AA:

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CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX
XX
SQ Sequence 150 AA;

Query Match 100.0%; Score 41; DB 3; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 GHRPLDK 7
Db 45 GHRPLDK 51
|||||

RESULT 32
AAM78493
ID AAM78493 standard; protein; 453 AA.
XX
XX AC AAM78493;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human protein SEQ ID NO 1155.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
XX OS
XX WO200157190-A2.
XX PN
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX PR
XX 27-APR-2000; 2000US-00560875.
XX PR
XX 20-JUN-2000; 2000US-00598075.
XX PR
XX 19-JUL-2000; 2000US-00620325.
XX PR
XX 01-SEP-2000; 2000US-00654936.
XX PR
XX 15-SEP-2000; 2000US-00663561.
XX PR
XX 20-OCT-2000; 2000US-00693325.
XX PR
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX PA
XX
XX Tang YT, Liu C, Drmanac RT, Aaundi V, Zhou P, Xu C, Cao Y;
XX PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX DR
XX N-PSDB; AAKS1626.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX
XX Claim 20; Page 3390-3391; 6221pp; English.

```

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 141 AA;

Query Match 100.0%; Score 41; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 GHRPLDK 7
DB 41 GHRPLDK 47
|||||||

RESULT 31
AAG00150
ID AAG00150 standard; protein; 150 AA.
XX
AC AAG00150;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 4231.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
DR N-PSDB; AAC00156.
DR
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 13; SEQ ID NO 4231; 71pp + Sequence Listing; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number of
XX 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX tissues. EST sequences usually correspond mainly to the 3' untranslated
XX region (UTR) of the mRNA because they are often obtained from oligo-dT
XX primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
XX sequences derived from the 5' ends of mRNAs and even in those cases where
XX longer cDNA sequences have been obtained, the full 5' UTR is rarely
XX included. 5' ESTs are derived from mRNAs with intact 5' ends and can
XX therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
XX are also used in diagnostic, forensic, gene therapy and chromosome
XX mapping procedures.

XX SQ Sequence 453 AA;
 Query Match 100.0%; Score 41; DB 4; Length 453;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 |||||
 Db 45 GHRPLDK 51

XX SQ Sequence 455 AA;
 Query Match 100.0%; Score 41; DB 8; Length 455;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 |||||
 Db 45 GHRPLDK 51

RESULT 34
 ABM85150
 ID ABM85150 standard; protein; 455 AA.
 XX AC ABM85150;
 XX DT 18-NOV-2004 (first entry)
 XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:5399.
 XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX OS Homo sapiens.
 XX PN WO2004023973-A2.
 XX PD 25-MAR-2004.
 XX PF 12-SEP-2003; 2003WO-US028227.
 XX PR 12-SEP-2002; 2002US-0410259P.
 XX PR 12-SEP-2002; 2002US-0410260P.
 XX PA (INCY-) INCYTE CORP.
 XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Hartshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patry S, Shi X, Suarez CJ;
 XX WPI; 2004-329368/30.
 DR N-PSDB; ACN43801.
 XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX PS Claim 27; Page; 190pp; English.
 XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX SQ Sequence 455 AA;

Query Match 100.0%; Score 41; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 45 GHRPLDK 51

RESULT 35
ABM85152
ID ABM85152 standard; protein; 474 AA.
XX AC ABM85152;
XX DT 18-NOV-2004 (first entry)
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:5401.
XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX OS Homo sapiens.
XX PN WO2004023973-A2.
XX PD 25-MAR-2004.
XX PF 12-SEP-2003; 2003WO-US028227.
XX PR 12-SEP-2002; 2002US-0410259P.
XX PR 12-SEP-2002; 2002US-0410260P.
XX PA (INCY-) INCYTE CORP.
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Fatury S, Shi X, Suarez CU;
XX WPI; 2004-329368/30.
DR N-PSDB; ACN43804.
XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX PS Claim 27; Page; 190pp; English.
XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders, endocrine
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX SQ Sequence 474 AA;

Query Match 100.0%; Score 41; DB 8; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 45 GHRPLDK 51

RESULT 36
ABM84478
ID ABM84478 standard; protein; 474 AA.
XX AC ABM84478;
XX DT 18-NOV-2004 (first entry)
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4727.
XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX OS Homo sapiens.
XX PN WO2004023973-A2.
XX PD 25-MAR-2004.
XX PF 12-SEP-2003; 2003WO-US028227.
XX PR 12-SEP-2002; 2002US-0410259P.
XX PR 12-SEP-2002; 2002US-0410260P.
XX PA (INCY-) INCYTE CORP.
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Fatury S, Shi X, Suarez CU;
XX WPI; 2004-329368/30.
DR N-PSDB; ACN43130.
XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX PS Claim 27; Page; 190pp; English.
XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders, endocrine
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX SQ Sequence 474 AA;

Query Match

100.0%; Score 41; DB 8; Length 474;

Best Local Similarity 100.0%; Pred. No. 2.7;		Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 GHRPLDK 7	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DB	45 GHRPLDK 51		
RESULT 37			
ABM84481	ID ABM84481 standard; protein; 474 AA.		
XX	AC	ABM84481;	
XX	DT	18-NOV-2004 (first entry)	
XX	DE	Human diagnostic and therapeutic pprotein SEQ ID NO:4730.	
XX	KW	gene therapy; human diagnostic and therapeutic polynucleotide; dithp.	
XX	OS	Homo sapiens.	
XX	PN	WO2004023973-A2.	
XX	PD	25-MAR-2004.	
XX	PF	12-SEP-2003; 2003WO-US028227.	
XX	PR	12-SEP-2002; 2002US-0410259P.	
XX	PR	12-SEP-2002; 2002US-0410260P.	
XX	PA	(INCY-) INCYTE CORP.	
XX	PI	Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;	
XX	PI	Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;	
XX	PI	Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;	
XX	PI	Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;	
XX	PI	Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;	
XX	PI	Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;	
XX	PI	Xu Y, Kwong M, Pollicky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;	
XX	PI	Fatury S, Shi X, Suarez CJ;	
XX	DR	WPI: 2004-329368/30.	
XX	DR	N-PSDB; ACM43133.	
XX	PT	New diagnostic and therapeutic polynucleotides and polypeptides, useful	
XX	PT	in diagnosing a condition, disease or disorder associated with human	
XX	PT	molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or	
XX	PT	in gene mapping.	
XX	PS	Claim 27; Page; 190pp; English.	
XX	CC	The invention relates to novel diagnostic and therapeutic polynucleotides	
XX	CC	selected from one of the 2722 sequences defined in the specification. A	
XX	CC	polynucleotide of the invention may have a use in gene therapy. The human	
XX	CC	diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be	
XX	CC	used to diagnose a particular condition, disease or disorder associated	
XX	CC	with human molecules, e.g. cell proliferative disorders,	
XX	CC	autoimmune/inflammatory disorder, developmental disorder, endocrine	
XX	CC	disorder, neurological disorders, gastrointestinal disorders, or	
XX	CC	infections caused by virus, bacteria, fungi or parasite. The dithp	
XX	CC	molecules may also be used in genetic mapping, in identifying individuals	
XX	CC	from minute biological samples, in detecting single nucleotide	
XX	CC	polymorphisms, as molecular weight markers, and for somatic or germline	
XX	CC	gene therapy. The present sequence represents a dithp protein of the	
XX	CC	invention. Note: The sequence data for this patent is not represented in	
XX	CC	the printed specification, but was obtained in electronic format directly	
XX	CC	from WIPO at www.wipo.int/pct/en/sequences/listing.htm	
XX	CC	Sequence 474 AA;	
Query Match		100.0%; Score 41; DB 8; Length 474;	
Best Local Similarity		100.0%; Pred. No. 2.7;	
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

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QY      1 GHRPLDK 7
Db      |||||
        45 GHRPLDK 51

RESULT 39
ABM85151
ID ABM85151 standard; protein; 474 AA.
XX
AC ABM85151;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5400.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JB, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro RA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Fatury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN43803.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 474 AA;

Query Match      100.0%; Score 41; DB 8; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GHRPLDK 7
Db      |||||
        45 GHRPLDK 51

RESULT 40
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ID ADE76868 standard; protein; 488 AA.
XX
AC ADE76868;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human protein expressed in a liver disorder #11.
XX
KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
KW tumour; liver; inflammatory disorder; immune response disorder;
KW high-throughput screening; differential gene expression; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003108871-A1.
XX
PD 12-JUN-2003.
XX
PF 30-JUL-2001; 2001US-00919039.
XX
PR 28-JUL-2000; 2000US-0222113P.
XX
PA (KASE/) KASER M R.
XX
PI Kaser MR;
XX
XX WPI; 2004-031227/03.
DR N-PSDB; ADE76867.
XX
XX Composition comprising several cDNAs that are differentially expressed in
PT treated human C3A liver cell cultures, useful for treating liver
PT disorders.
XX
XX Claim 1; SEQ ID NO 33; 41pp; English.
XX
XX The invention relates to a composition comprising several cDNAs that are
CC differentially expressed in a liver disorder. The composition is useful
CC for treating liver disorder such as hyperlipidaemia, hypertension, type
CC II diabetes, tumours of the liver and disorders of the inflammatory and
CC immune response. The composition is useful for a high-throughput method
CC of screening several molecules or compounds to identify a ligand which
CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
CC high-throughput method for using a protein to screen several molecules or
CC compounds to identify at least one ligand which specifically binds the
CC protein which involves combining the protein encoded by the cDNA with
CC several of molecules or compounds under conditions to allow specific
CC binding, and detecting specific binding between the protein and a
CC molecule or compound, therefore identifying a ligand which specifically
CC binds the protein. The composition is useful for detecting and
CC quantifying differential gene expression, can be used in gene therapy, to
CC formulate prognosis and to design a treatment regimen and to monitor the
CC efficacy of treatment. The present sequence represents the amino acid
CC sequence of a protein encoded by a cDNA differentially expressed in a
CC liver disorder.
XX
SQ Sequence 488 AA;

Query Match      100.0%; Score 41; DB 8; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GHRPLDK 7
Db      |||||
        42 GHRPLDK 48
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Search completed: June 1, 2005, 11:48:07
Job time : 115.467 secs

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OM protein - protein search, using sw model

Run on: June 1, 2005, 11:44:05 ; Search time 87.2667 Seconds
(without alignments)
27.728 Million cell updates/sec.

Title: US-09-424-940A-1
Perfect score: 41
Sequence: 1 GHRPLDK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues
Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %	Score	Match	Length	ID	Description
1	41	100.0	14	16	US-10-450-073-6	Sequence 6, Appli
2	41	100.0	20	14	US-10-142-935-6	Sequence 6, Appli
3	41	100.0	25	14	US-10-142-935-4	Sequence 4, Appli
4	41	100.0	28	16	US-10-459-030B-294	Sequence 294, App
5	41	100.0	30	14	US-10-131-543-5	Sequence 5, Appli
6	41	100.0	30	14	US-10-131-546-5	Sequence 5, Appli
7	41	100.0	30	14	US-10-131-346-5	Sequence 5, Appli
8	41	100.0	30	15	US-10-415-024-5	Sequence 5, Appli
9	41	100.0	87	15	US-10-276-774-1709	Sequence 33, Appl
10	41	100.0	488	10	US-09-919-039-33	Sequence 6, Appli
11	41	100.0	491	14	US-10-017-724-6	Sequence 9, Appli
12	36	87.8	10	14	US-10-142-935-9	Sequence 8, Appli
13	36	87.8	15	14	US-10-142-935-8	Sequence 8, Appli

14	36	87.8	16	15	US-10-378-674-7	Sequence 7, Appli
15	36	87.8	20	14	US-10-142-935-5	Sequence 5, Appli
16	36	87.8	479	16	US-10-437-963-127165	Sequence 127165, A
17	36	87.8	732	14	US-10-156-761-12627	Sequence 12627, A
18	36	87.8	735	16	US-10-437-963-182675	Sequence 182675, A
19	35	85.4	74	15	US-10-424-599-175814	Sequence 175814, A
20	35	85.4	240	14	US-10-017-161-1358	Sequence 1358, Ap
21	35	85.4	305	14	US-10-017-161-450	Sequence 450, App
22	35	85.4	305	14	US-10-017-161-468	Sequence 468, App
23	35	85.4	305	14	US-10-025-806-104	Sequence 104, App
24	35	85.4	305	15	US-10-292-798-404	Sequence 404, App
25	35	85.4	305	15	US-10-292-798-418	Sequence 418, App
26	35	85.4	305	15	US-10-041-615-2	Sequence 2, Appli
27	35	85.4	1052	15	US-10-236-417-156	Sequence 156, App
28	35	85.4	1052	15	US-10-236-417-164	Sequence 164, App
29	35	85.4	1071	16	US-10-322-281-857	Sequence 857, App
30	35	85.4	1112	15	US-10-236-417-158	Sequence 158, App
31	35	85.4	1182	16	US-10-322-281-860	Sequence 860, App
32	35	85.4	1203	9	US-09-799-875-5	Sequence 5, Appli
33	35	85.4	1203	15	US-10-649-156-5	Sequence 160, App
34	35	85.4	1273	15	US-10-236-417-160	Sequence 162, App
35	35	85.4	1321	15	US-10-236-417-162	Sequence 7, Appli
36	35	85.4	1369	15	US-10-288-798-7	Sequence 183296, A
37	35	85.4	1369	15	US-10-362-892-7	Sequence 236642, A
38	33	80.5	60	16	US-10-437-963-183296	Sequence 240543, A
39	33	80.5	76	15	US-10-424-599-236642	Sequence 240547, A
40	33	80.5	157	15	US-10-424-599-240543	Sequence 14386, A
41	33	80.5	231	15	US-10-424-599-240547	Sequence 9250, App
42	33	80.5	368	14	US-10-156-761-14386	Sequence 226, App
43	33	80.5	837	15	US-10-369-493-9250	Sequence 58001, A
44	32	78.0	68	15	US-10-220-120-226	
45	32	78.0	134	16	US-10-767-701-58001	

ALIGNMENTS

RESULT 1
US-10-450-073-6
; Sequence 6, Application US/10450073
; Publication NO. US20040132969A1
; GENERAL INFORMATION:
; APPLICANT: Melvin, William T
; APPLICANT: Thompson, William D
; APPLICANT: Stirr, Christina M
; TITLE OF INVENTION: Antibodies, Peptides, Analogs and Uses Thereof
; FILE REFERENCE: 0380-P03213USO
; CURRENT APPLICATION NUMBER: US/10/450,073
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/05505
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: GB 0030309.9
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesised
US-10-450-073-6

Query Match 100.0%; Score 41; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
Db 1 GHRPLDK 7
RESULT 2

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US-10-142-935-6
; Sequence 6, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-6

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Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
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RESULT 3
US-10-142-935-4
; Sequence 4, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-4

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Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 15 GHRPLDK 21

RESULT 4
US-10-459-030B-294
; Sequence 294, Application US/10459030B
; Publication No. US20040192596A1
; GENERAL INFORMATION:
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: A35859 PCT USA A 071986.0248
; CURRENT APPLICATION NUMBER: US/10/459,030B
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/AT01/00387
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: AT 2063/2000
; PRIOR FILING DATE: 2000-12-12

US-10-142-935-5
; Sequence 5, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-543-5

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US-10-131-546-5
; Sequence 5, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
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US-10-459-030B-294
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Best Local Similarity 100.0%; Pred. No. 0.66;
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QY 1 GHRPLDK 7
Db 1 GHRPLDK 7
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RESULT 5
US-10-131-543-5
; Sequence 5, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
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; LOCATION: 30
US-10-131-543-5
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Query Match      100.0%; Score 41; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 4 GHRPLDK 10
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RESULT 6
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; Sequence 5, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
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Best Local Similarity 100.0%; Pred. No. 0.7;
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Db      4 GHRPLDK 10

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; Publication No. US20030103899A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-346-5

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Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GHRPLDK 7
Db      4 GHRPLDK 10

RESULT 8
US-10-415-024-5
; Sequence 5, Application US/10415024
; Publication No. US20040058984A1
; GENERAL INFORMATION:
; APPLICANT: Diatide, Inc.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-015W01
; CURRENT APPLICATION NUMBER: US/10/415,024
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-346-5

Query Match          100.0%; Score 41; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GHRPLDK 7
Db      4 GHRPLDK 10

RESULT 9
US-10-276-774-1709
; Sequence 1709, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1709
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(87)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-276-774-1709

Query Match          100.0%; Score 41; DB 15; Length 87;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GHRPLDK 7
Db      31 GHRPLDK 37

RESULT 10
US-09-919-039-33
; Sequence 33, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
```

; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 3393861CD1
US-09-919-039-33

Query Match 100.0%; Score 41; DB 10; Length 488;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 42 GHRPLDK 48

RESULT 11
US-10-017-724-6
; Sequence 6, Application US/10017724
; Publication No. US2003009959A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-004
; CURRENT APPLICATION NUMBER: US/10/017,724
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/329,958
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-017-724-6

Query Match 100.0%; Score 41; DB 14; Length 491;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 12
US-10-142-935-9
; Sequence 9, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-9

Query Match 100.0%; Score 36; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 11 GHRPLD 16

Query Match 87.8%; Score 36; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 5 GHRPLD 10

RESULT 13
US-10-142-935-8
; Sequence 8, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-8

Query Match 87.8%; Score 36; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 10 GHRPLD 15

RESULT 14
US-10-378-674-7
; Sequence 7, Application US/10378674
; Publication No. US20040006209A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATIVE
; FILE REFERENCE: P07556US01/BAS
; CURRENT APPLICATION NUMBER: US/10/378,674
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/361,324
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-378-674-7

Query Match 87.8%; Score 36; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 11 GHRPLD 16

```

; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12627
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12627

Query Match      87.8%; Score 36; DB 14; Length 732;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 344 GHRPLD 349
|||||

RESULT 18
US-10-437-963-182675
; Sequence 182675, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 182675
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79840C.1.pap
US-10-437-963-182675

Query Match      87.8%; Score 36; DB 16; Length 735;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 94 GHRPLD 99
|||||

RESULT 19
US-10-424-599-175814
; Sequence 175814, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 175814
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79840C.1.pap
US-10-424-599-175814

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/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 175814
/ LENGTH: 74
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(74)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_129779C.1.pap
US-10-424-599-175814

Query Match      85.4%; Score 35; DB 15; Length 74;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 HRPDLK 7
Db      41 HRPDLK 46

RESULT 20
US-10-017-161-1358
/ Sequence 1358, Application US/10017161
/ Publication No. US20030143668A1
/ GENERAL INFORMATION:
/ APPLICANT: SUWA, MAKIKO
/ APPLICANT: ASAI, KIYOSHI
/ APPLICANT: AKIYAMA, YUTAKA
/ APPLICANT: ABURATANI, HIROYUKI
/ TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
/ FILE REFERENCE: 084335/0152
/ CURRENT APPLICATION NUMBER: US/10/017,161
/ CURRENT FILING DATE: 2002-12-18
/ PRIOR APPLICATION NUMBER: JP 2001/246789
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 2430
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1358
/ LENGTH: 240
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (8)..(41)
/ OTHER INFORMATION: Variable amino acid
US-10-017-161-1358

Query Match      85.4%; Score 35; DB 14; Length 240;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 HRPDLK 7
Db      155 HRPDLK 160

RESULT 21
US-10-017-161-450
/ Sequence 450, Application US/10017161
/ Publication No. US20030143668A1
/ GENERAL INFORMATION:
/ APPLICANT: SUWA, MAKIKO
/ APPLICANT: ASAI, KIYOSHI
/ APPLICANT: AKIYAMA, YUTAKA
/ APPLICANT: ABURATANI, HIROYUKI
/ TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
/ FILE REFERENCE: 084335/0152
/ CURRENT APPLICATION NUMBER: US/10/017,161
```

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/ CURRENT FILING DATE: 2002-12-18
/ PRIOR APPLICATION NUMBER: JP 2001/246789
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 2430
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 450
/ LENGTH: 305
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-017-161-450

Query Match      85.4%; Score 35; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 HRPDLK 7
Db      220 HRPDLK 225

RESULT 22
US-10-017-161-468
/ Sequence 468, Application US/10017161
/ Publication No. US20030143668A1
/ GENERAL INFORMATION:
/ APPLICANT: SUWA, MAKIKO
/ APPLICANT: ASAI, KIYOSHI
/ APPLICANT: AKIYAMA, YUTAKA
/ APPLICANT: ABURATANI, HIROYUKI
/ TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
/ FILE REFERENCE: 084335/0152
/ CURRENT APPLICATION NUMBER: US/10/017,161
/ CURRENT FILING DATE: 2002-12-18
/ PRIOR APPLICATION NUMBER: JP 2001/246789
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 2430
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 468
/ LENGTH: 305
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-017-161-468

Query Match      85.4%; Score 35; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 HRPDLK 7
Db      220 HRPDLK 225

RESULT 23
US-10-023-806-104
/ Sequence 104, Application US/10025806
/ Publication No. US20030198955A1
/ GENERAL INFORMATION:
/ APPLICANT: Li, Li
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Colman, Steven
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Casman, Stacie
/ APPLICANT: Edinger, Shlomit
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Sciore, Paul
/ APPLICANT: Smithson, Glennnda
/ APPLICANT: Peyman, John
/ APPLICANT: MacDougall, John
/ APPLICANT: Stone, David
/ APPLICANT: Vernet, Corine
/ APPLICANT: Shepoy, Suresh
```


APPLICANT: Gunther, Erik
APPLICANT: Millet, Isabelle
APPLICANT: Tchernev, Velizar
APPLICANT: Anderson, David
APPLICANT: Gusev, Vladimir
APPLICANT: Malyankar, Uriel
APPLICANT: Zhong, Haihong
APPLICANT: Ellerman, Karen
APPLICANT: Wolenc, Adam
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-224 AB
CURRENT APPLICATION NUMBER: US/10/025,806
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256,635
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/259,743
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/299,327
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 60/261,498
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/263,689
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/276,464
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/271,021
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/275,946
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/278,150
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/285,718
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 60/312,902
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/257,876
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/260,718
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/284,591
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 352
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 104
LENGTH: 305
TYPE: PRT
ORGANISM: Homo sapiens
US-10-025-806-104

Query Match 85.4%; Score 35; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HRPLDK 7
Db 220 HRPLDK 225

RESULT 24
US-10-292-798-404
Sequence 404, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 404
LENGTH: 305
TYPE: PRT
ORGANISM: Homo sapiens
US-10-292-798-404

Query Match 85.4%; Score 35; DB 15; Length 305;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HRPLDK 7
Db 220 HRPLDK 225

RESULT 25
US-10-292-798-418
Sequence 418, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 418
LENGTH: 305
TYPE: PRT
ORGANISM: Homo sapiens
US-10-292-798-418

Query Match 85.4%; Score 35; DB 15; Length 305;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HRPLDK 7
Db 220 HRPLDK 225

RESULT 26
US-10-041-615-2
Sequence 2, Application US/10041615
Publication No. US20040014038A1
GENERAL INFORMATION:
APPLICANT: Casman, Stacie J
APPLICANT: Edinger, Shlomit R
APPLICANT: Ellerman, Karen
APPLICANT: Smithson, Glennda
APPLICANT: Kekuda, Ramesh
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: No. US20040014038A1 GPCR-Like Proteins and Nucleic Acids Encod
FILE REFERENCE: 21402-233-061
CURRENT APPLICATION NUMBER: US/10/041,615
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: 60/259,552
PRIOR FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: 60/260,544
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/277,405

```
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 2
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-615-2

Query Match      85.4%; Score 35; DB 15; Length 305;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 HRPLDK 7
Db      220 HRPLDK 225

RESULT 27
US-10-236-417-156
; Sequence 156, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442C
; CURRENT APPLICATION NUMBER: US/10/236,417
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: US60/318,430
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US60/322,781
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/318,184
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/361,663
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US60/396,412
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US60/322,636
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,817
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,816
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/323,519
; PRIOR FILING DATE: 2001-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 164
; LENGTH: 1052
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-417-164

Query Match      85.4%; Score 35; DB 15; Length 1052;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GHRPLDK 7
Db      809 GHRPLSK 815

RESULT 28
US-10-322-281-857
; Sequence 857, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 857
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-322-281-857

Query Match      85.4%; Score 35; DB 16; Length 1071;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GHRPLDK 7
Db      798 GHRPLSK 804

RESULT 30
US-10-236-417-158
; Sequence 158, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
```

GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442C
; CURRENT APPLICATION NUMBER: US/10/236,417
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: US60/318,430
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US60/322,781
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/318,184
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/361,653
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US60/396,412
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US60/322,636
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,817
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,816
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/323,519
; PRIOR FILING DATE: 2001-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 158
; LENGTH: 1112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-417-158

Query Match 85.4%; Score 35; DB 15; Length 1112;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 809 GHRPLSK 815

RESULT 31
US-10-322-281-860
; Sequence 860, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 860
; LENGTH: 1182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-860

Query Match 85.4%; Score 35; DB 16; Length 1182;
Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 718 GHRPLSK 724

RESULT 32

US-09-799-875-5
; Sequence 5, Application US/09799875
; Patent No. US20020034780A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. US20020034780A1el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-875-5

Query Match 85.4%; Score 35; DB 9; Length 1203;
Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 799 GHRPLSK 805

RESULT 33
US-10-649-156-5
; Sequence 5, Application US/10649156
; Publication No. US20040038346A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. US20040038346A1el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/10/649,156
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: US/09/799,875
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-649-156-5

Query Match 85.4%; Score 35; DB 15; Length 1203;
Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 799 GHRPLSK 805

RESULT 34
US-10-236-417-160
; Sequence 160, Application US/10236417
; Publication No. US20040048256A1

; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442C
; CURRENT APPLICATION NUMBER: US/10/236,417
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: US60/318,430
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US60/322,781
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/318,184
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/361,663
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US60/396,412
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US60/322,636
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,817
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,816
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/323,519
; PRIOR FILING DATE: 2001-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 160
; LENGTH: 1273
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-417-160

Query Match 85.4%; Score 35; DB 15; Length 1273;
Best Local Similarity 85.7%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 809 GHRPLSK 815

RESULT 35
US-10-236-417-162
; Sequence 162, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442C
; CURRENT APPLICATION NUMBER: US/10/236,417
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: US60/318,430
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US60/322,781
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/318,184
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/361,663
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US60/396,412
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US60/322,636
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,817
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,816
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/323,519

; PRIOR FILING DATE: 2001-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 162
; LENGTH: 1321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-417-162

Query Match 85.4%; Score 35; DB 15; Length 1321;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 857 GHRPLSK 863

RESULT 36
US-10-288-798-7
; Sequence 7, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Daniel B.;
; APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;
; APPLICANT: RAMKUMAR, Jayalakmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 1369
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030207299A1 1989319CD1
US-10-288-798-7

Query Match 85.4%; Score 35; DB 15; Length 1369;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 905 GHRPLSK 911

RESULT 37

US-10-362-892-7
; Sequence 7, Application US/10362892
; Publication No. US20040038881A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga
; APPLICANT: NGUYEN, Daniel B.; WALIA, Narinder K.
; APPLICANT: HAPALIA, April J.A.; YAO, Monique G.
; APPLICANT: GANDHI, Ameena R.; GURURAJAN, Rajagopal
; APPLICANT: DING, Li; PATTERSON, Chandra S.
; APPLICANT: YUE, Henry; BAUGHN, Mariah R.
; APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael B.
; APPLICANT: ELLIOTT, Vicki S.; LU, Yan
; APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.
; APPLICANT: LAL, Preeti G.; RAMKUMAR, Jayalaxmi
; APPLICANT: WARREN, Bridget A.; KEARNEY, Liam
; APPLICANT: POLICKY, Jennifer L.; THANGAVELU, Kavitha
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PP-0209 USN
; CURRENT APPLICATION NUMBER: US/10/362,892
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 1369
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040038881A1 1989319CD1

US-10-362-892-7

Query Match 85.4%; Score 35; DB 15; Length 1369;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 905 GHRPLSK 911

RESULT 38

US-10-437-963-183296
; Sequence 183296, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 183296
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(60)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_80400C.1.pap
; US-10-437-963-183296

Query Match 80.5%; Score 33; DB 16; Length 60;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 46 GHRPLDK 52

RESULT 39

US-10-424-599-236642
; Sequence 236642, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 236642
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_55714C.1.pap
; US-10-424-599-236642

Query Match 80.5%; Score 33; DB 15; Length 76;
Best Local Similarity 85.7%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 1 GHRPLDK 7

RESULT 40

US-10-424-599-240543
; Sequence 240543, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240543
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(157)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59238C.1.pep
US-10-424-599-240543

Query Match 80.5%; Score 33; DB 15; Length 157;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLD 6
||:||||
Db 100 GHRPLD 105

Search completed: June 1, 2005, 11:57:09
Job time : 87.2667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 11:41:15 ; Search time 22.4 Seconds
(without alignments)
30.068 Million cell updates/sec

Title: US-09-424-940A-1

Perfect score: 41

Sequence: 1 GHRPLDK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Pir1:*
- 2: Pir2:*
- 3: Pir3:*
- 4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	31	2 A05297	fibrinogen beta ch
2	41	100.0	491	1 FGHUB	fibrinogen beta ch
3	36	87.8	201	2 C95399	probable transcrip
4	36	87.8	468	1 FGBOB	fibrinogen beta ch
5	36	87.8	1490	2 T47840	multi resistance p
6	35	85.4	463	2 A38463	fibrinogen beta ch
7	34	82.9	673	2 T40817	zinc finger protei
8	34	82.9	795	2 A84608	hypothetical prote
9	33	80.5	225	2 A75550	Mut7/nudix family
10	33	80.5	1058	2 D82654	ankyrin-like prote
11	32	78.0	423	2 T20233	hypothetical prote
12	32	78.0	476	2 E87040	acyl-CoA synthase
13	32	78.0	485	2 F70464	hypothetical prote
14	32	78.0	611	2 D84423	probable WD-40-rep
15	32	78.0	878	2 B17245	hypothetical prote
16	31	75.6	42	2 B92087	myelin basic prote
17	31	75.6	169	1 MBBOB	myelin basic prote
18	31	75.6	169	2 F72465	hypothetical prote
19	31	75.6	176	2 D86434	hypothetical prote
20	31	75.6	215	2 S23432	protein T17H7.16 [
21	31	75.6	225	2 T25957	pyroglutamyl-pepti
22	31	75.6	228	2 D83071	probable ATP-bindi
23	31	75.6	230	2 T46417	hypothetical prote
24	31	75.6	309	2 T19389	hypothetical prote
25	31	75.6	343	2 E71149	hypothetical prote
26	31	75.6	344	2 H87710	hypothetical prote
27	31	75.6	345	2 D96011	probable oxidoredu
28	31	75.6	374	2 S77072	queuine tRNA-ribos
29	31	75.6	424	2 C69077	thiamin biosynthes

30	31	75.6	473	2 G70607	probable fadD36 pr
31	31	75.6	480	2 G75072	prolyl-tRNA synthe
32	31	75.6	480	2 A71093	proline-tRNA ligas
33	31	75.6	548	2 C75499	cytidine/deoxycyti
34	31	75.6	633	2 E31265	ipaA protein - Shi
35	31	75.6	648	2 C83023	probable oxidoredu
36	31	75.6	1970	2 T03284	myoblast city prot
37	31	75.6	3670	2 T36249	CDA peptide synthe
38	30	73.2	50	1 INTO2	insulin 2 - toadfi
39	30	73.2	104	2 H83530	hypothetical prote
40	30	73.2	123	2 T15030	hypothetical prote
41	30	73.2	127	2 G95291	hypothetical prote
42	30	73.2	162	2 E87094	probable phosphope
43	30	73.2	184	2 A37041	homeotic protein A
44	30	73.2	202	2 AE3377	queuine tRNA-ribos
45	30	73.2	213	2 T35433	hypothetical prote

ALIGNMENTS

RESULT 1

A05297
fibrinogen beta chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C/Accession: B94308; A03123; A37512; A05297; B37512; D03118
Birken, S.; Wilner, G.D.; Canfield, R.E.
Thromb. Res. 7, 599-610, 1975
A/Title: Studies of the structure of canine fibrinogen.
A/Reference number: A94308; MUID:76081726; PMID:1198547
A/Accession: B94308
A/Molecule type: protein
A/Residues: 1-31 <BIR>

A/Cross-references: UNIPROT:P02677
R:Blomback, B.; Blomback, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A/Title: Studies on fibrinopeptides from mammals.
A/Reference number: A03118
A/Accession: A03123
A/Molecule type: protein
A/Residues: 1-19 <BLO>
R:Krajewski, T.; Blomback, B.
Acta Chem. Scand. 22, 1339-1346, 1968
A/Reference number: A37512; MUID:69066367; PMID:5727635
A/Accession: A37512
A/Molecule type: protein
A/Residues: 1-19 <KRA>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
C/Keywords: blood coagulation; liver; plasma; sulfoxprotein
F/1-19/Product: fibrinopeptide B #status experimental <APT>
F/2/Binding site: sulfate (Tyr) (covalent) #status experimental
F/3/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 100.0%; Score 41; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

Db 20 GHRPLDK 26

RESULT 2

FGHUB
fibrinogen beta chain precursor [validated] - human
N/Alternate names: coagulation factor I
N/Contains: fibrinopeptide B
C:Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C/Accession: B43568; A90469; B90469; I37389; A94433; A90437; A94309; G54223; A03121; B371
R/Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990

Annu. Rev. Biochem. 53, 195-229, 1984

A;Title: Fibrinogen and fibrin.

A;Reference number: A90041; MUID:84305751; PMID:6383194

A;Contents: annotation; review, EM structure, polymerization, ligands

R;Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.

Ann. N. Y. Acad. Sci. 408, 449-456, 1983

A;Title: Cloning of fibrinogen genes and their cDNA.

A;Reference number: A90038; MUID:83254384; PMID:6575700

A;Contents: annotation

R;Kirschbaum, N.E.; Budzynski, A.Z.

J. Biol. Chem. 265, 13659-13676, 1990

A;Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-ter

A;Reference number: A37117; MUID:90337977; PMID:2143188

A;Contents: annotation; hementin cleavage site

A;Note: hementin, a protease from Haementeria ghilianii, the giant South American leech,

C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves

ization sites responsible for the formation of the soft clot.

C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliz

ger) and between alpha chains (weaker) of different monomers.

C;Comment: All fibrinogen chains are synthesized in the liver.

C;Genetics:

A;Gene: GDB:FCB

A;Cross-references: GDB:119130; OMIM:134830

A;Map position: 4q28-4q28

A;Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2

C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FCF

ins are contained in the core. Two three-chain coiled coils emerge from this core and cor

from the distal domain nodes.

C;Function:

A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into f

A;Pathway: blood coagulation

C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfid

C;Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglutamic aci

F;1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>

F;31-491/Product: fibrinogen beta chain #status experimental <NAI>

F;31-44/Product: fibrinopeptide B #status experimental <APT>

F;45-491/Product: fibrin beta chain #status experimental <PGB>

F;45-47/Region: polymerization site

F;95-228/Domain: fibrinogen disulfide ring homology <FDR>

F;238-487/Domain: fibrinogen beta/gamma homology <PBG>

F;31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment

F;44-45/Cleavage site: Arg-Gly (thrombin) #status experimental

F;95/Disulfide bonds: interchain (to alpha-55) #status experimental

F;106/Disulfide bonds: interchain (to alpha-68) #status experimental

F;110/Disulfide bonds: interchain (to gamma-45) #status experimental

F;223/Disulfide bonds: interchain (to alpha-184) #status experimental

F;227/Disulfide bonds: interchain (to gamma-161) #status experimental

F;231-316,241-270,424-437/Disulfide bonds: #status experimental

F;394/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 41; DB 1; Length 491;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

DB 45 GHRPLDK 51

|||||

|||||

RESULT 3

C95399

probable transcription regulator [imported] - Sinorhizobium meliloti (strain 1021) magap1

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: C95399

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: C95399

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-201 <CUR>

A;Cross-references: UNIPROT:Q92XY9; CB:AE006469; PIDN:AAK65757.1; PID:g14524255; GSPDB:G
 A;Experimental source: strain 1021, megaplasmid pSymA
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 P.; D., J.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: Sma2008
 A;Genome: plasmid

Query Match 87.8%; Score 36; DB 2; Length 201;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6

Db 175 GHRPLD 180

RESULT 4

FGB0B

fibrinogen beta chain - bovine
 N;Contains: fibrinopeptide B
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 13-Sep-1996
 C;Accession: A03122; B03117; B37507; A37513; S02443
 R;Blomback, B.; Doolittle, R.F.
 Acta Chem. Scand. 17, 1816-1819, 1963
 A;Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
 A;Reference number: A03122
 A;Accession: A03122
 A;Molecule type: protein
 A;Residues: 1-4 <SLQ>
 R;Sjoquist, J.; Blomback, B.; Wallen, P.
 Ark. Kemi 16, 425-436, 1960
 A;Title: Amino acid sequence of bovine fibrinopeptides.
 A;Reference number: A03117
 A;Accession: B03117
 A;Molecule type: protein
 A;Residues: 5-21 <SUQ>
 R;Martinielli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S.
 Arch. Biochem. Biophys. 192, 27-32, 1979
 A;Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrin
 A;Reference number: A37507; MUID:79164394; PMID:434821
 A;Accession: B37507
 A;Molecule type: protein
 A;Residues: 22-53 <MAR>
 R;Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
 A;Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
 A;Reference number: A37513; MUID:81199473; PMID:6262803
 A;Accession: A37513
 A;Molecule type: mRNA
 A;Residues: 44-468 <CHU>
 R;Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
 FEBS Lett. 232, 56-60, 1988
 A;Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to

A;Reference number: S02443; MUID:88211875; PMID:2966748

A;Accession: S02443

A;Molecule type: protein

A;Residues: 373-374 <MED>

C;Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
 C;Superfamily: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alpha
 C;Keywords: blood coagulation; glycoprotein; plasma; pyroglyutamic acid; sulfoprotein
 F;76-205/Domain: fibrinogen disulfide ring homology <FDR>
 F;215-464/Domain: fibrinogen beta/gamma homology <FBG>

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
 F;21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
 F;371/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match 87.8%; Score 36; DB 1; Length 468;
 Best Local Similarity 85.7%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

Db 22 GHRPYDK 28

RESULT 5

T47840

multi resistance protein homolog - Arabidopsis thaliana
 N;Alternate names: protein T209.140
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C;Accession: T47840
 R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
 submitted to the Protein Sequence Database, February 2000
 A;Reference number: Z24475
 A;Accession: T47840
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1490 <NYA>
 A;Cross-references: UNIPROT:Q9M1C7; EMBL:AL138658
 A;Experimental source: cultivar Columbia; BAC clone T209
 C;Genetics:

A;Map position: 3

A;Introns: 9/1; 795/3; 824/3; 1036/3; 1075/3; 1174/1; 1245/3; 1347/3; 1369/1; 1449/1

A;Note: T209.140

C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
 Query Match 87.8%; Score 36; DB 2; Length 1490;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6

Db 1226 GHRPLD 1231

RESULT 6

A38463

fibrinogen beta chain - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004

C;Accession: A38463

R;Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.

Biochemistry 30, 3290-3294, 1991

A;Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage site

A;Reference number: A38463; MUID:91182745; PMID:2009266

A;Accession: A38463

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-463 <WEI>

C;Cross-references: UNIPROT:Q02020; GB:M58514; NID:g211779; PIDN:AAA48770.1; PID:g211780
 C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
 F;73-202/Domain: fibrinogen disulfide ring homology <FDR>
 F;212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 85.4%; Score 35; DB 2; Length 463;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPDLK 7

Db 19 HRPDLK 24

```
RESULT 7
T40817
zinc finger protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40817
R;Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z21949
A;Accession: T40817
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-673 <BEC>
A;Cross-references: UNIPROT:O94271; EMBL:AL032684; PIDN:CAA21808.1; GSPDB:GN00067; SPDB:
A;Experimental source: strain 972h-; clone p1 p8B7
C;Genetics:
A;Gene: SPDB:SPBP8B7.23
A;Map position: 2
F;210-278/Domain: 2 RING finger homology <RRN>

Query Match      82.9%; Score 34; DB 2; Length 673;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
||| |||
160 GHRPMDK 166

RESULT 8
A84608
hypothetical protein At2g22020 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: A84608
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84608
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-795 <STO>
A;Cross-references: UNIPROT:Q9S1Z7; GB:AE002093; NID:g4417294; PIDN:AAD20419.1; GSPDB:GN
C;Genetics:
A;Gene: At2g22020
A;Map position: 2

Query Match      82.9%; Score 34; DB 2; Length 795;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
41 GHRPLER 47

RESULT 9
A75550
MutR/nudix family protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: A75550
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75550
```

```
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-225 <WHI>
A;Cross-references: UNIPROT:Q9RXW3; GB:AE001881; GB:AE000513; NID:g6457853; PIDN:AAF0977;
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0192
A;Map position: 1
C;Superfamily: NUDIX hydrolase

Query Match      80.5%; Score 33; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
178 GHRPLDK 184

RESULT 10
D82654
ankyrin-like protein XF1640 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82654
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: D82654
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1058 <SIM>
A;Cross-references: UNIPROT:Q9PCW4; GB:AE003991; GB:AE003849; NID:g9106696; PIDN:AAF8444;
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; AJ
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigre
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tshakoto, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1640

Query Match      80.5%; Score 33; DB 2; Length 1058;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
|||||
497 GHRPVD 502

RESULT 11
T20233
hypothetical protein C54G4.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20233
R;Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19241
A;Accession: T20233
A;Status: preliminary; translated from GB/EMBL/DBJ
```

A:Molecule type: DNA
A:Residues: 1-423 <WIL>
A:Cross-references: UNIPROT:Q18847; EMBL:Z755533; PIDN:CAA99815.1.; GSPDB:GN00019; CESP:CS
A:Experimental source: clone C54G4
C:Genetics:
A:Gene: CESP:C54G4.2
A:Map position: 1
A:Introns: 76/3; 172/3; 272/2; 312/1; 367/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C54G4.2

Query Match 78.0%; Score 32; DB 2; Length 423;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
Db 197 HRPLDK 202
|||||

RESULT 12
E87040
acyl-CoA synthase [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: E87040
R: Cole, S.T.; Eiglmeier, K.; Parthill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: E87040
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-476 <STO>
A:Cross-references: UNIPROT:Q50017; GB:AL450380; NID:gl3093059; PIDN:CAC31432.1; GSPDB:G
A:Gene: xcic
C:Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology

Query Match 78.0%; Score 32; DB 2; Length 476;
Best Local Similarity 57.1%; Pred. No. 83;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 271 GHRPIER 277
|||||

RESULT 13
F70464
hypothetical protein aq_1912 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: F70464
R: Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: F70464
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-485 <AQF>
A:Cross-references: UNIPROT:O67746; GB:AE000763; NID:g2984178; PIDN:AAC07717.1; PID:g298
A:Experimental source: strain VF5
C:Genetics:
A:Gene: aq_1912

Query Match 78.0%; Score 32; DB 2; Length 485;
Best Local Similarity 85.7%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 18 GDRPLDK 24
|||||

RESULT 14

D84423

Probable WD-40-repeat protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: D84423

R: Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: D84423
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-611 <STO>
A:Cross-references: UNIPROT:Q9ZU34; GB:AE002093; NID:g4262240; PIDN:AAD14533.1; GSPDB:GN
C:Genetics:
A:Gene: At2g01330
A:Map position: 2

Query Match 78.0%; Score 32; DB 2; Length 611;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 408 GHQPLD 413
|||||

RESULT 15

T17245

hypothetical protein DKFZp586J0917.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T17245

R: Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18722

A:Accession: T17245

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-878 <KOE>

A:Cross-references: EMBL:AL117455

A:Experimental source: adult uterus; clone DKFZp586J0917

C:Genetics:

A:Note: DKFZp586J0917.1

Query Match 78.0%; Score 32; DB 2; Length 878;

Best Local Similarity 71.4%; Pred. No. 1.6e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 403 GHRPLSR 409
|||||

RESULT 16

B92087

myelin basic protein - rabbit (fragment)

N:Alternate names: myelin A1 protein

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 30-Sep-1993

C:Accession: B92087; A03140

R: Shapira, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.

J. Biol. Chem. 246, 4630-4640, 1971

A:Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine

A;Reference number: A92087
 A;Accession: B92087
 A;Molecule type: protein
 A;Residues: 1-42 <SHA>
 C;Superfamily: myelin basic protein
 C;Keywords: myelin

Query Match 75.6%; Score 31; DB 2; Length 42;
 Best Local Similarity 71.4%; Pred. NO. 10;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 |||||:

DB 31 GHRPQDE 37

RESULT 17

MBBOB

myelin basic protein - bovine
 N;Alternate names: myelin A1 protein
 N;Contains: myelin peptide amide-12 (MPA-12); myelin peptide amide-16 (MPA-16)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 18-Dec-1981 #sequence revision 18-Dec-1981 #text change 09-Jul-2004
 C;Accession: A92089; A92160; A92087; S54343; A61641; A03140
 R;Eylar, E.H.; Brostoff, S.; Hashim, G.; Caccam, J.; Burnett, P.
 J. Biol. Chem. 246, 5770-5784, 1971
 A;Title: Basic A1 protein of the myelin membrane. The complete amino acid sequence.
 A;Reference number: A92089; MUID:72007306; PMID:5096093
 A;Accession: A92089
 A;Molecule type: protein
 A;Residues: 1,'S',2-169 <EYL>
 A;Cross-references: UNIPROT:P02687
 R;Brostoff, S.W.; Reuter, W.; Hitchens, M.; Eylar, E.H.
 J. Biol. Chem. 249, 559-567, 1974
 A;Title: Specific cleavage of the A1 protein from myelin with cathepsin D.
 A;Reference number: A92160; MUID:74070688; PMID:4129204
 A;Accession: A92160

A;Molecule type: protein
 A;Residues: 1-169 <BRO>
 R;Shapira, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.
 J. Biol. Chem. 246, 4630-4640, 1971
 A;Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine
 A;Reference number: A92087
 A;Accession: A92087
 A;Molecule type: protein
 A;Residues: 43-87 <SHA>
 R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
 Biochem. J. 306, 551-555, 1995
 A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glia
 A;Reference number: S54343; MUID:95194333; PMID:7887910
 A;Accession: S54343
 A;Molecule type: protein
 A;Residues: 74-75,'HG',78-82,'D',84-88;105,'X',107-108,'X',110-114,'X',116-119 <OKA>
 R;Takamatsu, K.; Tatemoto, K.
 Neurochem. Res. 17, 239-246, 1992

A;Title: Isolation and characterization of two novel peptide amides originating from myelin
 A;Reference number: A61641; MUID:92319189; PMID:1377792
 A;Accession: A61641
 A;Molecule type: protein
 A;Residues: 1-12 <TAK>
 A;Accession: B61641
 A;Residues: 1-16 <TA2>
 A;Note: these peptides have carboxyl-terminal amides probably produced by a non-enzymatic
 R;Brostoff, S.; Eylar, E.H.
 Proc. Natl. Acad. Sci. U.S.A. 68, 765-769, 1971
 A;Title: Localization of methylated arginine in the A1 protein from myelin.
 A;Reference number: A93777; MUID:71153946; PMID:4994464
 A;Contents: annotation

A;Note: Arg-106 is modified to monomethylarginine and dimethylarginine
 R;Eylar, E.H.; Caccam, J.; Jackson, J.J.; Westall, F.C.; Robinson, A.B.
 Science 168, 1220-1223, 1970
 A;Title: Experimental allergic encephalomyelitis: synthesis of disease-inducing site of

A;Reference number: A94241; MUID:70178977; PMID:5442707

A;Contents: annotation
 A;Note: the region including residues 114-122 induces experimental allergic encephalomyel
 C;Superfamily: myelin basic protein
 C;Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephal
 F;1-169/Product: myelin basic protein #status experimental <MAT>
 F;1-16/Product: myelin peptide amide-12 #status experimental <PA16>
 F;1-12/Product: myelin peptide amide-12 #status experimental <PA12>
 F;1/Modified site: acetylated amino end (Ala) #status experimental
 F;12/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide amic
 F;16/Modified site: amidated carboxyl end (Ala) (amide in mature form myelin peptide amic
 F;106/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg) (f

Query Match 75.6%; Score 31; DB 1; Length 169;
 Best Local Similarity 71.4%; Pred. NO. 44;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 |||||:

DB 76 GHRPQDE 82

RESULT 18

F72465

hypothetical protein APE2369 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence revision 20-Aug-1999 #text change 09-Jul-2004

C;Accession: F72465

R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: F72465

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-169 <KAW>

A;Cross-references: UNIPROT:Q9Y9B8; DDBJ:AP000064; NID:G5105945; PIDN:BA81382.1; PID:G51

A;Experimental source: strain K1

C;Genetic:

A;Gene: APE2369

C;Superfamily: Aeropyrum pernix hypothetical protein APE2369

Query Match 75.6%; Score 31; DB 2; Length 169;
 Best Local Similarity 71.4%; Pred. NO. 44;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 |||||:

DB 100 GYRPLDE 106

RESULT 19

D86434

protein T17H7.16 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text change 09-Jul-2004

C;Accession: D86434

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D86434

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-176 <STO>

A;Cross-references: UNIPROT:Q9SY30; GB:AE005172; NID:g4926831; PIDN:AND32941.1; GSPDB:GN
 C;Genetics:
 A;Gene: T17H7.16
 A;Map position: 1

Query Match 75.6%; Score 31; DB 2; Length 176;
 Best Local Similarity 57.1%; Pred. No. 46;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 ||:|:
 Db 2 GHKPK 8

RESULT 20
 pyroglutamyl-peptidase I (EC 3.4.19.3) pcp - Bacillus subtilis
 N;Alternate names: 5-oxoprol-1-peptidase; pyrrolidone-carboxylate peptidase pcp
 C;Species: Bacillus subtilis
 C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S23432; G69673
 R;Awade, A.; Cleuziat, P.; Gonzales, T.; Robert-Baudouy, J.
 FEBS Lett. 305, 67-73, 1992
 A;Title: Characterization of the pcp gene encoding the pyrrolidone carboxyl peptidase of
 A;Reference number: S23432; MUID:92339527; PMID:1353026
 A;Accession: S23432
 A;Molecule type: DNA
 A;Residues: 1-215 <AWA>
 A;Cross-references: UNIPROT:P28618; EMBL:X66034; NID:g40036; PIDN:CAA46833.1; PID:g40037
 A;Experimental source: strain 168
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berta
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.
 Koester, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
 akuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Toseato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, K.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A;Reference number: A69580; MUID:9804033; PMID:9384377
 A;Accession: G69673
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-215 <KUN>
 A;Cross-references: GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12059.1; PID:g2632551
 A;Experimental source: strain 168
 C;Genetics:
 A;Gene: pcp; pep
 C;Superfamily: pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase)
 C;Keywords: hydrolase; omega peptidase

Query Match 75.6%; Score 31; DB 2; Length 215;
 Best Local Similarity 57.1%; Pred. No. 58;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 ||:|:
 Db 97 GHQPID 103

RESULT 21
 T25957
 hypothetical protein ZC204.11 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T25957
 R;Wamsley, P.; Kramer, J.

submitted to the EMBL Data Library, December 1996
 A;Description: The sequence of C. elegans cosmid ZC204.
 A;Reference number: Z20116
 A;Accession: T25957
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-225 <WAM>
 A;Cross-references: UNIPROT:P91542; EMBL:U80839; PIDN:AAB37923.1; GSPDB:GN000020; CESP:ZC
 C;Genetics:
 A;Gene: CESP:ZC204.11
 A;Map position: 2
 A;Introns: 28/2; 55/3; 87/3; 133/1

Query Match 75.6%; Score 31; DB 2; Length 225;
 Best Local Similarity 71.4%; Pred. No. 60;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 ||:|:
 Db 54 GHTPLDE 60

RESULT 22

D83071
 Probable ATP-binding component of ABC transporter PA4594 [imported] - Pseudomonas aeruginosa
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C;Accession: D83071
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 A;Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: D83071
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-228 <STO>
 A;Cross-references: UNIPROT:Q9HVJ2; GB:AE004873; GB:AE004091; NID:g9950839; PIDN:AAG0798
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA4594

Query Match 75.6%; Score 31; DB 2; Length 228;
 Best Local Similarity 83.3%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLD 6
 ||:|:
 Db 136 GHRPAD 141

RESULT 23

T46417
 hypothetical protein DKFP434K1323.1 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 C;Accession: T46417
 R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A;Reference number: Z23034
 A;Accession: T46417
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-250 <AAA>
 A;Cross-references: UNIPROT:Q9NSV7; EMBL:AL137714
 A;Experimental source: adult testis; clone DKFP434K1323
 C;Genetics:
 A;Note: DKFP434K1323.1

Query Match 75.6%; Score 31; DB 2; Length 250;
 Best Local Similarity 83.3%; Pred. No. 68;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7

|||||

Db 178 HRPLDE 183

RESULT 24

T19389

hypothetical protein C18D11.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004

C:Accession: T19389

R:Barlow, K.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19118

A:Accession: T19389

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-309 <WIL>

A:Cross-references: UNIPROT:Q9XT22; EMBL:Z92826; PIDN:CAB07322.1; GSPDB:GN00021; CESP:CI

A:Experimental source: clone C18D11

C:Genetics:

A:Gene: CESP:C18D11.4

A:Map position: 3

A:Introns: 17/3; 39/2; 146/3; 241/2

C:Superfamily: ribonucleoprotein repeat homology

Query Match 75.6%; Score 31; DB 2; Length 309;

Best Local Similarity 83.3%; Pred. No. 85;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLD 6

|||||

Db 279 GHRPYD 284

RESULT 25

E71149

hypothetical protein PH0407 - *Pyrococcus horikoshii*

C:Species: *Pyrococcus horikoshii*

C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004

C:Accession: E71149

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: E71149

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-343 <RAW>

A:Cross-references: UNIPROT:O58144; GB:AP000002; MUID:G3236129; PIDN:BAA29482.1; PID:G325

A:Experimental source: strain OT3

A>Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH0407

Query Match 75.6%; Score 31; DB 2; Length 343;

Best Local Similarity 71.4%; Pred. No. 95;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

|||||

Db 106 GHRPFLK 112

RESULT 26

H87710

hypothetical protein CC3722 [imported] - *Caulobacter crescentus*

C:Species: *Caulobacter crescentus*

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: H87710

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of *Caulobacter crescentus*.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: H87710

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-344 <STO>

A:Cross-references: UNIPROT:Q9A244; GB:AE005673; MUID:g13425492; PIDN:AAK25684.1; GSPDB:G

C:Genetics:

A:Gene: CC3722

C:Superfamily: phosphoglycerate dehydrogenase

Query Match 75.6%; Score 31; DB 2; Length 344;

Best Local Similarity 71.4%; Pred. No. 95;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

|||||

Db 332 GHRPPDR 338

RESULT 27

D96011

probable oxidoreductase protein SMB20648 [imported] - *Sinorhizobium meliloti* (strain 102)

C:Species: *Sinorhizobium meliloti*

C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: D96011

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo

A:Reference number: A95842; MUID:21396508; PMID:11481431

A:Accession: D96011

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-345 <KUR>

A:Cross-references: UNIPROT:Q92TY7; GB:AL591985; PIDN:CAC49756.1; PID:g15141243; GSPDB:G

A:Experimental source: strain 1021, megaplasmid pSymB

R:Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.

A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: SMB20648

A:Genome: plasmid

C:Superfamily: fission yeast pyridoxine 4-dehydrogenase

Query Match 75.6%; Score 31; DB 2; Length 345;

Best Local Similarity 71.4%; Pred. No. 95;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

|||||

Db 10 GHRPLGR 16

RESULT 28

S77072

queuine tRNA-ribosyltransferase (EC 2.4.2.29) - *Synechocystis* sp. (strain PCC 6803)

N:Alternate names: protein slr0713; transfer RNA-guanine transglycosylase

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S77072

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
A;Accession: G70607
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S77072
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-374 <KAN>
A;Cross-references: UNIPROT:Q55983; EMBL:D64005; GB:AB001339; NID:q1001779; PIDN:BAAL076
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: tgc
A;Start codon: GTG
C;Function:
A;Description: catalyzes the exchange of guanine base in the first anticodon position of
A;Pathway: queuosine biosynthesis; tRNA modification
C;Superfamily: queuine tRNA-ribosyltransferase
C;Keywords: glycosyltransferase; pentosyltransferase; tRNA modification

Query Match 75.6%; Score 31; DB 2; Length 374;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPDLK 7
|||||
Db 303 HRPDLDE 308

RESULT 29
C69077
thiamin biosynthesis protein thic MTH1576 - Methanobacterium thermoautotrophicum (strain
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69077
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Ji, Wani, N.
ki S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: C69077
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-424 <MTH>
A;Cross-references: UNIPROT:O27617; GB:AE000917; GB:AE000666; NID:92622689; PIDN:AA88604
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1576
A;Start codon: GTG
C;Superfamily: thiamin biosynthesis protein thic

Query Match 75.6%; Score 31; DB 2; Length 424;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 267 GHMPLDQ 273

RESULT 30
G70607
probable fadD36 protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: G70607
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: G70607
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-473 <COL>
A;Cross-references: UNIPROT:O05295; GB:293777; GB:AL123456; NID:g3261726; PIDN:CAB07836
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: fadD36
C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
F;42-469/Domain: acetate-CoA ligase homology <ACL>

Query Match 75.6%; Score 31; DB 2; Length 473;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 268 GHRPVER 274

RESULT 31
G75072
prolyl-tRNA synthetase (pros) PAB1724 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G75072
R;anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: G75072
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-480 <KAW>
A;Cross-references: UNIPROT:Q3V022; GB:AJ248286; GB:AL096836; NID:95458366; PIDN:CAB4988
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1724
C;Superfamily: proline-tRNA ligase pros

Query Match 75.6%; Score 31; DB 2; Length 480;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLD 6
|||||
Db 96 GHEPLD 101

RESULT 32
A71093
proline-tRNA ligase (EC 6.1.1.15) - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: A71093
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatai, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: A71093
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-480 <KAW>
A;Cross-references: UNIPROT:O58734; GB:AP000004; NID:g3236131; PIDN:BAA30103.1; PID:g323
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1006
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 75.6%; Score 31; DB 2; Length 480;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLD 6
|||
Db 96 GHEPLD 101

RESULT 33

C75499
cytidine/deoxycytidylate deaminase/nudix/methyltransferase domains protein - Deinococcus
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: C75499
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: C75499
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-548 <WHI>
A:Cross-references: UNIPROT:Q9RWR3; GB:AE001918; GB:AE000513; NID:g6458294; PIDN:AAF1018
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0603
A:Map position: 1

Query Match 75.6%; Score 31; DB 2; Length 548;
Best Local Similarity 71.4%; Pred. NO. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 159 GHRPEDR 165

RESULT 34

E31265
ipaA protein - Shigella flexneri plasmid
C:Species: Shigella flexneri
C>Date: 31-Mar-1990 #sequence_revision 26-Apr-1996 #text_change 09-Jul-2004
C:Accession: S12763; E31265
R;Venkatesan, M.M.; Buysse, J.M.
Nucleic Acids Res. 18, 1648, 1990
A:Title: Nucleotide sequence of invasion plasmid antigen gene ipaA from Shigella flexneri
A:Reference number: S12763; MUID:90221912; PMID:2183200
A:Accession: S12763
A:Molecule type: DNA
A:Residues: 1-633 <VEN>
A:Cross-references: UNIPROT:P18010; EMBL:X17628; NID:g47030; PIDN:CAA35624.1; PID:g47031
R;Venkatesan, M.M.; Buysse, J.M.; Kopecko, D.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 9317-9321, 1988
A:Title: Characterization of invasion plasmid antigen genes (ipaBCD) from Shigella flexneri
A:Reference number: A94219; MUID:89057927; PMID:3057506
A:Accession: E31265
A:Molecule type: DNA
A:Residues: 1-88 <VE2>
A:Cross-references: GB:J04117; NID:g152740; PIDN:AAA26525.1; PID:g551981
C:Genetics:
A:Gene: ipaA
A:Genome: plasmid

Query Match 75.6%; Score 31; DB 2; Length 633;
Best Local Similarity 83.3%; Pred. NO. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
|||||
Db 417 GHRPLN 422

RESULT 35

C83023
probable oxidoreductase PA4986 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: C83023
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brj
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C83023
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-648 <STO>
A:Cross-references: UNIPROT:Q9HUH9; GB:AE004911; GB:AE004091; NID:g9951264; PIDN:AAG08371
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA4986
C:Superfamily: Methylophilus methylotrophus W3A1 trimethylamine dehydrogenase

Query Match 75.6%; Score 31; DB 2; Length 648;
Best Local Similarity 57.1%; Pred. NO. 1.9e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 605 GHQPVDK 611

RESULT 36

T03284
myoblast city protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03284
R;Erickson, M.R.S.; Galletta, B.J.; Abmayr, S.M.
J. Cell Biol. 138, 589-603, 1997
A:Title: Drosophila myoblast city encodes a conserved protein that is essential for myob
A:Reference number: Z14881; MUID:97392689; PMID:9245788
A:Accession: T03284
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1970 <ERI>
A:Cross-references: UNIPROT:Q9VCH4; EMBL:AF007805; NID:g2367443; PID:g2367444
C:Genetics:
A:Gene: mbc
A:Cross-references: FlyBase:FBgn0015513
A:Map position: 3

Query Match 75.6%; Score 31; DB 2; Length 1970;
Best Local Similarity 57.1%; Pred. NO. 6.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 490 GHQPIDE 496

RESULT 37

T36249
CDA peptide synthetase II SCB63.02c [imported] - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 12-Jul-2004
C:Accession: T36249
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21602
A:Accession: T36249
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3670 <SAU>

A;Cross-references: UNIPROT:Q924X5; EMBL:AL035640; PIDN:CAB38517.1; GSPDB:GN00070; SCORE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: cdaP2; SCORDB:SC63.02c
C;Superfamily: non-ribosomal peptide synthetase; acetate-CoA ligase homology; acyl carrier
C;Keywords: carrier protein; phosphopantetheine; phosphoprotein
F;512-932/Domain: acetate-CoA ligase homology <ACL1>
F;948-1016/Domain: acyl carrier protein homology <ACP1>
F;1545-1981/Domain: acetate-CoA ligase homology <ACL2>
F;1997-2085/Domain: acyl carrier protein homology <ACP2>
F;2608-3064/Domain: acetate-CoA ligase homology <ACP3>
F;3080-3147/Domain: acyl carrier protein homology <ACP3>
F;980,2029,3112/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 75.6%; Score 31; DB 2; Length 3670;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLD 6
|||||
Db 578 GHRPTD 583

RESULT 38
INTO2
insulin 2 - toadfish (tentative sequence)
C;Species: Batrachoididae gen. sp. (toadfish)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C;Accession: A01605
R;Smith, L.F.
Am. J. Med. 40, 662-666, 1966
A;Title: Species variation in the amino acid sequence of insulin.
A;Reference number: A90029; MUID:66160119; PMID:5949593
A;Accession: A01605
A;Molecule type: protein
A;Residues: 1-29;30-50 <SMI>
A;Cross-references: UNIPROT:P01338
C;Superfamily: insulin
C;Keywords: hormone; pancreas
F;1-29/Domain: insulin chain B #status experimental <BCH>
F;1-29,30-50/Product: insulin #status experimental <MAT>
F;30-50/Domain: insulin chain A #status experimental <ACH>
F;8-36,20-49,35-40/Disulfide bonds: #status predicted

Query Match 73.2%; Score 30; DB 1; Length 50;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDK 7
|||||
Db 37 HRPCDK 42

RESULT 39
H83530
hypothetical protein PA0922 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83530
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-104 <STO>
A;Cross-references: UNIPROT:Q91535; GB:AE004526; GB:AE004091; NID:G9946819; PIDN:AAG0431
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0922

Query Match 73.2%; Score 30; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLD 6
|||||
Db 61 HRPLD 65

RESULT 40
T15030
hypothetical protein Y115 - Yersinia pestis plasmid pMT1
C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15030
R;Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid
A;Reference number: Z18268; MUID:99043898; PMID:9826348
A;Accession: T15030
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-123 <LIN>
A;Cross-references: UNIPROT:Q9ZGY0; EMBL:AF074611; NID:G3883003; PID:G3883113; PIDN:AA08
C;Genetics:
A;Gene: Y115
A;Genome: plasmid pMT1
C;Superfamily: Yersinia pestis plasmid pMT1 hypothetical protein Y115

Query Match 73.2%; Score 30; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPL 5
|||||
Db 21 GHRPL 25

Search completed: June 1, 2005, 11:52:52
Job time : 24.4 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 11:40:35 ; Search time 105 Seconds
(without alignments)
34.139 Million cell updates/sec

Title: US-09-424-940A-1
Perfect score: 41
Sequence: 1 GHRPLDK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	31	1 FIBB CANFA	P02677 canis famil
2	41	100.0	491	1 FIBB HUMAN	P02675 homo sapien
3	37	90.2	404	2 Q9VA50	Q9VA50 drosophila
4	36	87.8	58	2 Q8MVT2	Q8MVT2 myxine glut
5	36	87.8	159	2 Q8E1G4	Q8E1G4 streptococc
6	36	87.8	159	2 Q8E6V1	Q8E6V1 streptococc
7	36	87.8	201	2 Q92XV9	Q92XV9 rhizobium m
8	36	87.8	238	2 Q7MTW3	Q7MTW3 porphyromon
9	36	87.8	468	1 FIBB BOVIN	P02676 bos taurus
10	36	87.8	471	2 Q8SBA0	Q8SBA0 oryza sativ
11	36	87.8	471	2 Q7XC70	Q7XC70 oryza sativ
12	36	87.8	732	2 Q82D89	Q82D89 streptomyc
13	36	87.8	735	2 Q84E87	Q84E87 oryza sativ
14	36	87.8	1490	2 Q9M1C7	Q9M1C7 arabidopsis
15	35	85.4	120	1 YH42 COXBU	Q83AY5 coxiella bu
16	35	85.4	305	1 Q4F5 HUMAN	Q8NH21 homo sapien
17	35	85.4	305	1 Q4FH HUMAN	Q8NGA8 homo sapien
18	35	85.4	390	2 Q81VM8	Q81VM8 homo sapien
19	35	85.4	463	1 FIBB CHICK	Q02020 gallus gall
20	35	85.4	479	1 FIBB RAT	F14480 rattus norv
21	35	85.4	481	2 Q8K0E8	Q8K0E8 mus musculu
22	35	85.4	503	2 Q7TME5	Q7TME5 rattus norv
23	35	85.4	505	2 Q9HA50	Q9HA50 homo sapien
24	35	85.4	598	2 Q6P3R6	Q6P3R6 homo sapien
25	35	85.4	643	2 Q641L5	Q641L5 mus musculu
26	35	85.4	959	2 Q46S83	Q46S83 desulfovibr
27	35	85.4	1052	2 Q6ZQ09	Q6ZQ09 mus musculu
28	35	85.4	1311	2 Q6P4S6	Q6P4S6 mus musculu
29	35	85.4	1345	2 Q6CH64	Q6CH64 yarrowia li
30	35	85.4	1371	2 Q9Y2K2	Q9Y2K2 homo sapien
31	34	82.9	417	1 MUAJ_THETN	Q8Y9G7 thermoanaer

RESULT 1

FIBB CANFA ID FIBB CANFA STANDARD; PRT; 31 AA.

AC P02677; DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN Name=FGB;

OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]

RP MEDLINE=69081726; PubMed=1198547; DOI=10.1016/0049-3848(75)90106-1;
RA Birken S., Wilner G.D., Canfield R.E.;

RT "Studies of the structure of canine fibrinogen."
RL Thromb. Res. 7:599-610(1975).
RN [2]

RP SEQUENCE OF 1-19.

RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals."
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [3]

RP SEQUENCE OF 1-19.

RX MEDLINE=69086367; PubMed=5727635;

RA Krajewski T., Blomback B.;

RT "The location of tyrosine-O-sulphate in fibrinopeptides."
RL Acta Chem. Scand. 22:1339-1346(1968).

CC -I- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.

CC -I- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains

CC (alpha, beta and gamma), linked to each other by disulfide bonds.

CC -I- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,

CC which cleaves fibrinopeptides A and B from alpha and beta chains,

CC and thus exposes the N-terminal polymerization sites responsible

CC for the formation of the soft clot.

DR PIR; B94308; A05297.

DR InterPro; IPR002181; Fibrinogen C.

DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.

KW Blood coagulation; Direct protein sequencing; Plasma; Sulfation.

FT PEPTIDE 1 19 Fibrinopeptide B.

FT CHAIN 20 >31 Fibrinogen beta chain.

FT MOD_RES 2 2 Sulfotyrosine (partial).

FT MOD_RES 3 3 Sulfotyrosine.

FT NON_TER 31 31

SQ SEQUENCE 31 AA; 3731 MW; A043727257698156 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.49;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db |||||
20 GHRPLDK 26

RESULT 2
FIBB HUMAN
ID FIBB_HUMAN STANDARD; PRT; 491 AA.
AC P02675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
GN Name-FGB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
fibrinogen.";
RL Adv. Exp. Med. Biol. 281:39-48(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83283433; PubMed=6688356;
RA Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;
RT "Characterization of complementary deoxyribonucleic acid and genomic
deoxyribonucleic acid for the beta chain of human fibrinogen.";
RL Biochemistry 22:3244-3250(1983).
RN [3]
RP SEQUENCE FROM N.A.
RX Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
fibrinogen.";
RL (In) Liu C.Y., Chien S. (eds.);
RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48, Plenum
Press, New York (1991).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS SER-100; HIS-170; LEU-265 AND
LYS-478.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-
PHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>)";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
structural variants.";
RL (In) Peeters H. (eds.);
RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
Pergamon Press, Oxford (1980).
RN [6]
RP SEQUENCE OF 31-491.
RX MEDLINE=79124640; PubMed=420779;
RA Watt K.W.K., Takagi T., Doolittle R.F.;
RT "Amino acid sequence of the beta chain of human fibrinogen.";
RL Biochemistry 18:68-76(1979).
RN [7]
RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.
RX MEDLINE=76225080; PubMed=936108; DOI=10.1016/0049-3848(76)90245-0;
RA Blomback B., Hessel B., Hogg D.;
RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RL Thromb. Res. 8:639-658(1976).
RN [8]
RP SEQUENCE OF 1-38 FROM N.A.
RX MEDLINE=87146483; PubMed=3029722;
RA Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z.,
RA Marguerie G.;
RT "Characterization of the 5'-flanking region for the human fibrinogen
beta gene.";
RL Nucleic Acids Res. 15:1615-1625(1987).
RN [9]
RP SEQUENCE OF 31-44.
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).
RN [10]
RP REVIEW, AND DISULFIDE BONDS.
RX MEDLINE=83254370; PubMed=6575689;
RA Henschen A., Lottspeich F., Kehl M., Southan C.;
RT "Covalent structure of fibrinogen.";
RL Ann. N. Y. Acad. Sci. 408:28-43(1983).
RN [11]
RP DISULFIDE BONDS.
RX MEDLINE=77245999; PubMed=891553;
RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
RT "Primary structure of human fibrinogen. Characterization of disulfide-
containing cyanogen-bromide fragments.";
RL Eur. J. Biochem. 77:595-610(1977).
RN [12]
RP DISULFIDE BONDS.
RX Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
RA Cassman K.G., Goldbaum D.M., Doolittle L.K., Friesner S.J.;
RT "The structures of fibrinogen and fibrin.";
RL (In) Magnusson S., Ottessen M., Foltmann B., Dano K., Neurath H.
(eds.);
RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
Pergamon Press, New York (1978).
RN [13]
RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RX MEDLINE=84305751; PubMed=6383194;
RA Doolittle R.F.;
RT "Fibrinogen and fibrin.";
RL Annu. Rev. Biochem. 53:195-229(1984).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
RX MEDLINE=97472408; PubMed=9333233; DOI=10.1038/38947;
RA Spraggon G., Evere S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its
crosslinked counterpart from fibrin.";
RL Nature 389:455-462(1997).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
RX MEDLINE=98292395; PubMed=9628725; DOI=10.1021/bi9804129;
RA Evere S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
different bound ligands.";
RL Biochemistry 37:8637-8642(1998).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 164-491.
RX MEDLINE=99175089; PubMed=10074346; DOI=10.1021/bi982626w;
RA Evere S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human
fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RL Biochemistry 38:2941-2946(1999).
RN [17]
RP INTERACTION WITH FBLN1.
RX MEDLINE=95370284; PubMed=7642629; DOI=10.1074/jbc.270.33.19459;
RA Tran H., Tanaka A., Litvinovich S.V., Medved L.V., Haudenschild C.C.,
RA Argaves W.S.;
RT "The interaction of fibulin-1 with fibrinogen. A potential role in
hemostasis and thrombosis.";
RL J. Biol. Chem. 270:19458-19464(1995).
RN [18]
RP VARIANT BALTIMORE-2 LYS-478.
RX MEDLINE=890588942; PubMed=3194892; DOI=10.1016/0049-3848(88)90096-5;
RA Schmelzer C.H., Ebert R.F., Bell W.R.;
RT "A polymorphism at B beta 448 of fibrinogen identified during
structural studies of fibrinogen Baltimore II.";
RL Thromb. Res. 52:173-177(1988).
RN [19]

RP VARIANT ISE ARG-45.
RX MEDLINE=91208409; PubMed=2018836;
RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
RA Asakura S., Shirakawa S.;
RT "A new congenital abnormal fibrinogen Ise characterized by the
RT replacement of B beta glycine-15 by cysteine.";
RL Blood 77:1958-1963(1991).
RN [20]
RP VARIANT NAPLES THR-98.
RX MEDLINE=92340664; PubMed=1634610;
RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
RT "Molecular basis of fibrinogen Naples associated with defective
RT thrombin binding and thrombophilia. Homozygous substitution of B beta
RT 68 Ala-->Thr.";
RL J. Clin. Invest. 90:238-244(1992).
RN [21]
RP VARIANTS IJMUIDEN CYS-44 AND NIJMEGEN CYS-74.
RX MEDLINE=92228809; PubMed=1565641;
RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
RA Kerst A.P.J.A., Lord S.T.;
RT "Abnormal fibrinogens IJMuiden (B beta Arg14-->Cys) and Nijmegen (B
RT beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
RT complexes.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
RN [22]
RP VARIANT NEW YORK-1 39-GLY--LEU-102 DEL.
RX MEDLINE=85157605; PubMed=3156856;
RA Liu C.Y., Koehn J.A., Morgan F.J.;
RT "Characterization of fibrinogen New York 1. A dysfunctional fibrinogen
RT with a deletion of B beta(9-72) corresponding exactly to exon 2 of the
RT gene.";
RL J. Biol. Chem. 260:4390-4396(1985).
RN [23]
RP VARIANTS GLU-2; LEU-265 AND LYS-478.
RX MEDLINE=99318093; PubMed=10391209; DOI=10.1038/10290;
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nimesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions
RT of human genes.";
RL Nat. Genet. 22:231-238(1999).
RN [24]
RP ERRATUM.
RX PubMed=10545957;
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nimesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RL Nat. Genet. 23:373-373(1999).
RN [25]
RP VARIANTS CONGENITAL AFIBRINOGENEMIA ARG-383 AND ASP-430.
RX MEDLINE=20129589; PubMed=10666208;
RA Duga S., Asselta R., Santagostino E., Zinalli S., Simonc T.,
RA Malcovati M., Mannucci P.M., Turchini M.L.;
RT "Missense mutations in the human beta fibrinogen gene cause congenital
RT afibrinogenemia by impairing fibrinogen secretion.";
RL Blood 95:1336-1341(2000).
RN [26]
RP VARIANT CONGENITAL AFIBRINOGENEMIA CYS-196.
RX MEDLINE=21361164; PubMed=11468164; DOI=10.1182/blood.V98.3.661;
RN [27]
Query Match 100.0%; Score 41; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
Db 45 GHRPLDK 11
RESULT 3
Q9VA50

ID Q9VA50 PRELIMINARY; PRT; 404 AA.
AC Q9VA50;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE CG31013-PA.
GN ORFNames=CG31013;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfankuch C., Baldwin D.,
RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Rosler C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Paclab J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";


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RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaser P., Rusniok C., Buchrieser C., Chevalier P., Frangeul L.,
RA Meadek T., Zouine M., Couve E., Lalloui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513 (2002).
DR EMBL; AL766845; CAD46071.1; -.
DR Sagalish; G80427; -.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002481; FUR.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF01475; FUR; 1.
DR ProDom; PD002003; FUR; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 159 AA; 18584 MW; 31FBA715A358C127 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
DB 7 GHRPLD 12

RESULT 7
Q92XY9 PRELIMINARY; PRT; 201 AA.
AC Q92XY9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Putative transcriptional regulator.
GN ORFNames=SMa2008;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymA megaplasmid.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
CC 1- SIMILARITY: Contains 1 HTH tetr-type DNA-binding domain.
DR EMBL; AB007296; AAK65757.1; -.
DR FIR; C95399; C95399.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR001647; HTH_retr.
DR Pfam; PF00440; Tetr_N; 1.
DR PRINTS; PR00455; HTHSTR.
KW Complete proteome; DNA-binding; Plasmid; Transcription;
KW Transcription regulation.
SQ SEQUENCE 201 AA; 21500 MW; 447E9E9BF63EF551 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
DB 7 GHRPLD 12

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Db 175 GHRPLD 180

RESULT 8
Q7MTW3 PRELIMINARY; PRT; 238 AA.
AC Q7MTW3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=PG1818;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601 (2003).
DR EMBL; AB017178; AQA66816.1; -.
DR TIGR; PG1818; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 238 AA; 26945 MW; DCA6C728CE6C9448 CRC64;

Query Match 87.8%; Score 36; DB 2; Length 238;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 3 GHRPTDK 9

RESULT 9
FIBB_BOVIN STANDARD; PRT; 468 AA.
AC P02676;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
GN Name=FGB;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-4.
RA Blomback B., Doolittle R.F.;
RT "The sequence of amino acids at the N-terminal end of bovine
RT fibrinopeptide B.";
RL Acta Chem. Scand. 17:1816-1819 (1963).
RN [2]
RP SEQUENCE OF 5-21.
RA Sjoquist J., Blomback B., Wallen P.;
RT "Amino acid sequence of bovine fibrinopeptides.";
RL Ark. Kem. 16:425-436 (1960).
RN [3]
RP SEQUENCE OF 22-53.
RX MEDLINE=79164394; PubMed=434821;
RA Martinelli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,
RA Hurrell J.G.R., Leach S.J., Scheraga H.A.;

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RT "Amino acid sequences of portions of the alpha and beta chains of
 RL bovine fibrinogen.";
 Arch. Biochem. Biophys. 192:27-32(1979).
 [4]
 RN SEQUENCE OF 44-468 FROM N.A.
 RA MEDLINE=81199473; PubMed=6262803;
 Arch. Biochem. Biophys. 192:27-32(1979).
 RA "Characterization of a cDNA clone coding for the beta chain of bovine
 RT fibrinogen.";
 RT Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).
 CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
 CC (alpha, beta and gamma), linked to each other by disulfide bonds.
 CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot. The soft clot is converted
 CC into the hard clot by factor XIIIa which catalyzes the epsilon-
 CC (gamma-glutamyl)lysine cross-linking between gamma chains
 CC (stronger) and between alpha chains (weaker) of different
 CC monomers.
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; V00110; CAA23444.1; -;
 DR PDB; 1DEQ; X-ray; B/E/O/R=61-468.
 DR PDB; 1JY2; X-ray; O/R=61-116.
 DR PDB; 1JY3; X-ray; O/R=61-116.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
 DR 3D-structure; Blood coagulation; Direct protein sequencing;
 KW Glycoprotein; Plasma; Platelet; Pyrrolidone carboxylic acid;
 KW Sulfation.
 FT PEPTIDE 1 21 Fibrinopeptide B.
 FT CHAIN 22 468 Fibrinogen beta chain.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 6 6 Sulfotyrosine.
 FT SITE 21 22 Cleavage (by thrombin; release
 FT fibrinopeptide B).
 FT DISULFID 72 72 Interchain (with alpha).
 FT DISULFID 83 83 Interchain (with alpha).
 FT DISULFID 87 87 Interchain (with gamma).
 FT DISULFID 200 200 Interchain (with gamma).
 FT DISULFID 204 204 Interchain (with alpha).
 FT DISULFID 208 293 By similarity.
 FT DISULFID 218 247 By similarity.
 FT DISULFID 401 414 By similarity.
 FT CARBOHYD 371 371 N-linked (GlcNAc...) (Probable).
 FT STRAND 72 73
 FT TURN 77 79
 FT STRAND 81 84
 FT HELIX 86 112
 FT TURN 113 113
 SQ SEQUENCE 468 AA; 53340 MW; 2DED42F443AA4B37 CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 468;
 Best Local Similarity 85.7%; Pred. No. 90;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db 22 GHRPYDK 28

RESULT 10
 Q8SBAO PRELIMINARY; PRT; 471 AA.
 AC Q8SBAO;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein OSJNBa0042H09.17.
 GN Name=OSJNBa0042H09.17;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
 RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
 RA Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
 RA VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
 RA Salzberg S.L., White O., Fraser C.M.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Buell R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC079874; AAL79787.1; -;
 DR Gramene; Q8SBAO; -;
 DR GO; GO:0008415; F:Acyltransferase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002123; Acyltransferase.
 DR Pfam; PF01553; Acyltransferase; 1.
 DR SMART; SM00563; PlcC; 1.
 DR Hypothetical protein.
 KW SEQUENCE 471 AA; 50200 MW; 75D92E78D51937DD CRC64;
 Query Match 87.8%; Score 36; DB 2; Length 471;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLD 6
 Db 32 GHRPLD 37
 RESULT 11
 Q7XC70 PRELIMINARY; PRT; 471 AA.
 AC Q7XC70;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=OSJNBa0042H09.17;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice
 RT chromosome 10.";
 RL Science 300:1566-1569(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017119; AAF55004.1; -;
 DR Gramene; Q7XC70; -;

DR GO; GO:0008415; P:acyltransferase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002123; Acyltransferase.
 DR Pfam; PF01553; Acyltransferase; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 471 AA; 50200 MW; 75D92E78D51937DD CRC64;

Query Match 87.8%; Score 36; DB 2; Length 471;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
 DB 32 GHRPLD 37
 |||||

RESULT 12

Q82D89 PRELIMINARY; PRT; 732 AA.
 AC Q82D89;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative glycosyl transferase.
 GN OrderedLocusNames=SAV5093;
 OS Streptomyces avermitilis;
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomyceinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Complete genome sequence and comparative analysis of the industrial
 microorganism Streptomyces avermitilis.";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL; AP005041; BAC72805.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0047355; F:CDP-glycerol glycerophosphotransferase acti. . .; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0019350; P:teichoic acid biosynthesis; IEA.
 DR InterPro; IPR001173; Glyco.trans.2.
 DR InterPro; IPR007554; Glyphos.transf.
 DR Pfam; PF00535; Glycos.transf.2; 1.
 DR Pfam; PF04464; Glyphos.transf.1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 732 AA; 81912 MW; D6011953CA0C017C CRC64;

Query Match 87.8%; Score 36; DB 2; Length 732;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
 DB 344 GHRPLD 349
 |||||

RESULT 13

Q94E87 PRELIMINARY; PRT; 735 AA.
 ID Q94E87

AC Q94E87;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE B1045D11.13 protein.
 GN Name=B1045D11.13;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12447438; DOI=10.1038/nature01184;
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
 RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 RA Waki K., Yanagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1.";
 RL Nature 420:312-316(2002).
 DR EMBL; AP003199; BAB61147.1; -;
 DR Gramene; Q94E87; -;
 DR InterPro; IPR002885; PPR.
 DR InterPro; IPR008940; Prenyl.trans.
 DR Pfam; PF01535; PPR; 11.
 DR TIGRFAMs; TIGR00756; PPR; 7.
 SQ SEQUENCE 735 AA; 79897 MW; 540392FCBF125BF6 CRC64;
 Query Match 87.8%; Score 36; DB 2; Length 735;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
 DB 94 GHRPLD 99
 |||||

RESULT 14
 Q9M1C7 PRELIMINARY; PRT; 1490 AA.
 AC Q9M1C7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Multi resistance protein homolog.
 GN Name=R209.140;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nyakatura G., Fairmann B., Dauner D., Sterr W., Holland R.,
 RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quettier F.,
 RA Salanoubat M.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AL138658; CAB75931.1; -;

```
DR PIR; T47840; T47840.
DR HSP; P26361; IRO2.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005524; F: ATP binding; IEA.
DR GO; GO:0042626; F: ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F: nucleotide binding; IEA.
DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane1.
DR InterPro; IPR001140; ABC_TM_transpt.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00929; ABC_TM1F; 2.
DR PROSITE; PS0211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS0893; ABC_TRANSPORTER_2; 2.
KW ATP-binding.
SQ
Query Match 87.8%; Score 36; DB 2; Length 1490;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
DB 1226 GHRPLD 1231

RESULT 15
YH42_COXBU YH42_COXBU STANDARD; PRT; 120 AA.
ID AC Q83AY5;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical UPF0102 protein CB01742.
OS Coccidia burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OX NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile phase I / RSA 493;
RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
RA Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
RA Nelson W.C., Ward N.L., Tettelin H., Davidson T.M., Beanan M.J.,
RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
RA Thompson H.A., Samuel J.B., Fraser C.M., Heidelberg J.F.;
RT "Complete genome sequence of the Q-fever pathogen, Coxiella
RT burnetii";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
CC -!- SIMILARITY: Belongs to the UPF0102 family.
CC
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CC
CC EMBL; A5016965; AAO91236.1; -.
DR TIGR; CB01742; -.
DR HAMAP; MF00048; -.
DR InterPro; IPR003509; UPF0102.
DR Pfam; PF02021; UPF0102; 1.
DR TIGRPFams; TIGR00252; UPF0102; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 120 AA; 14231 MW; A41A98C6B80DAE33 CRC64;
```

```
Query Match 85.4%; Score 35; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
DB 88 HRPLDK 93

RESULT 16
O4F5_HUMAN O4F5_HUMAN STANDARD; PRT; 305 AA.
ID AC Q8NH21;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Olfactory receptor 4F5.
GN Homo-OR4F5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Putative odorant receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -!- DATABASE: NAME=Human Olfactory Receptor Data Explorer
CC (HORDE);
CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols";
CC
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CC
CC EMBL; AB065592; BAC05820.1; -.
DR Genew; HGNC:14825; OR4F5.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000725; Olfact_receptor.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Multigene family; Olfaction;
KW Transmembrane.
FT DOMAIN 1 18 Extracellular (Potential).
FT TRANSMEM 19 42 1 (Potential).
FT DOMAIN 43 50 Cytoplasmic (Potential).
FT TRANSMEM 51 72 2 (Potential).
FT DOMAIN 73 93 Extracellular (Potential).
FT TRANSMEM 94 113 3 (Potential).
FT DOMAIN 114 132 Cytoplasmic (Potential).
FT TRANSMEM 133 151 4 (Potential).
FT DOMAIN 152 188 Extracellular (Potential).
FT TRANSMEM 189 212 5 (Potential).
FT DOMAIN 213 228 Cytoplasmic (Potential).
FT TRANSMEM 229 251 6 (Potential).
FT DOMAIN 252 262 Extracellular (Potential).
FT TRANSMEM 263 282 7 (Potential).
FT DOMAIN 283 305 Cytoplasmic (Potential).
FT DISULFID 90 182 By similarity.
SQ SEQUENCE 305 AA; 34330 MW; 70E99D068AE2DD59 CRC64;
```

Query Match 85.4%; Score 35; DB 1; Length 305;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
 DB 220 HRPLDK 225

RESULT 17
 O4FH_HUMAN STANDARD; PRT; 305 AA.
 AC Q8VY8; PRELIMINARY; PRT; 390 AA.
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Olfactory receptor 4F17.
 GN Name=OR4F17; Synonyms=OR4F19;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 receptor genes."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Putative odorant receptor.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -!- DATABASES: NMB=Human Olfactory Receptor Data Explorer
 CC (HORDE);
 CC WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols";
 CC -----
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 CC -----
 CC EMBL; AB065917; BAC06132.1; -
 CC Genew; HGNC:15381; OR4F17.
 CC InterPro; IPR000276; GPCR Rhodopsin.
 CC InterPro; IPR000725; Olfact_receptor.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHOOPS.
 CC PRINTS; PR00245; OLFACTORYR.
 CC PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
 CC PROSITE; PS0262; G PROTEIN RECP F1_2; 1.
 CC G-protein coupled receptor; Multigene family; Olfaction;
 KW Transmembrane.
 FT DOMAIN 1 18 Extracellular (Potential).
 FT TRANSMEM 19 42 1 (Potential).
 FT DOMAIN 43 50 Cytoplasmic (Potential).
 FT TRANSMEM 51 72 2 (Potential).
 FT DOMAIN 73 93 Extracellular (Potential).
 FT TRANSMEM 94 113 3 (Potential).
 FT DOMAIN 114 132 Cytoplasmic (Potential).
 FT TRANSMEM 133 151 4 (Potential).
 FT DOMAIN 152 188 Extracellular (Potential).
 FT TRANSMEM 189 212 5 (Potential).
 FT DOMAIN 213 228 Cytoplasmic (Potential).
 FT TRANSMEM 229 251 6 (Potential).
 FT DOMAIN 252 262 Extracellular (Potential).
 FT TRANSMEM 263 282 7 (Potential).
 FT DOMAIN 283 305 Cytoplasmic (Potential).
 FT DISULFID 90 182 By similarity.
 SQ SEQUENCE 305 AA; 34212 MW; 2DDFAC5504EDFA6E CRC64;

Query Match 85.4%; Score 35; DB 1; Length 305;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
 DB 220 HRPLDK 225

RESULT 18
 Q8IYM8 PRELIMINARY; PRT; 390 AA.
 AC Q8IYM8;
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueudin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC035583; AAH35583.2; -
 KW Hypothetical protein.
 SQ SEQUENCE 390 AA; 42414 MW; 466BF7F6AEDA051C CRC64;

Query Match 85.4%; Score 35; DB 2; Length 390;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 DB 60 GHRPLDK 66

RESULT 19
 FIBB_CHICK STANDARD; PRT; 463 AA.
 AC Q02020;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]
 DE (Fragment).

GN Name=FGB;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
 RX MEDLINE=91182745; PubMed=2009266;
 RA Weissbach L., Oddoux C., Procyk R., Grieninger G.;
 RT "The beta chain of chicken fibrinogen contains an atypical thrombin
 cleavage site";
 RL Biochemistry 30:3290-3294(1991).
 CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
 polymerize into fibrin and acting as a cofactor in platelet
 aggregation.
 CC -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
 (alpha, beta and gamma), linked to each other by disulfide bonds.
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 which cleaves fibrinopeptides A and B from alpha and beta chains,
 and thus exposes the N-terminal polymerization sites responsible
 for the formation of the soft clot. The soft clot is converted
 into the hard clot by factor XIIIa which catalyzes the epsilon-
 (gamma-glutamyl)lysine cross-linking between gamma chains
 (stronger) and between alpha chains (weaker) of different
 monomers.
 CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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 CC
 DR EMBL; M58514; AAA48770.1; -;
 DR FIB; A38463; A38463.
 DR PDB; 1E13; X-ray; B/E=1-463.
 DR PDB; 1MJJ; X-ray; B/E=1-463.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; Fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 DR 3D-structure; Blood coagulation; Direct protein sequencing;
 KW Glycoprotein; Plasma; Platelet; Sulfation.
 FT NON_TER 1 1 Fibrinopeptide B.
 FT PEPTIDE <1 17 Fibrinogen beta chain.
 FT CHAIN 18 463 Sulfotyrosine (By similarity).
 FT MOD_RES 5 5 Cleavage (by thrombin; release
 FT SITE 17 18 fibrinopeptide B).
 FT DISULFID 69 69 Interchain (with alpha) (By similarity).
 FT DISULFID 80 80 Interchain (with alpha) (By similarity).
 FT DISULFID 84 84 Interchain (with gamma) (By similarity).
 FT DISULFID 197 197 Interchain (with alpha) (By similarity).
 FT DISULFID 201 201 Interchain (with gamma) (By similarity).
 FT DISULFID 205 289 By similarity.
 FT DISULFID 215 244 By similarity.
 FT DISULFID 397 410 By similarity.
 FT CARBOHYD 367 367 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 463 AA; 52678 MW; 2044CD49BA79EC7B CRC64;
 Query Match 85.4%; Score 35; DB 1; Length 463;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HRPLOK 7
 Db 19 HRPLOK 24
 RESULT 20

FIBB_RAT
 ID FIBB_RAT STANDARD; PRT; 479 AA.
 AC P14480;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
 GN Name=Fgb;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Sprague-Dawley; Tissue=Liver;
 MEDLINE=95143386; PubMed=7841303;
 RA Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.;
 RT "Cloning of the complete coding sequence of rat fibrinogen B beta
 chain cDNA: interspecies conservation of fibrin beta 15-42 primary
 structure";
 RL Blood Coagul. Fibrinolysis 5:487-496(1994).
 RN [2]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX MEDLINE=84194000; PubMed=6232608;
 RA Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
 RT "Potential basis for regulation of the coordinately expressed
 fibrinogen genes: homology in the 5' flanking regions";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
 RN [3]
 RP SEQUENCE OF 19-32.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 RN [4]
 RP SEQUENCE OF 183-479 FROM N.A.
 RX MEDLINE=89378771; PubMed=2673932; DOI=10.1016/0378-1119(89)90100-5;
 RA Eastman E.M., Gilula N.B.;
 RT "Cloning and characterization of a cDNA for the B beta chain of rat
 fibrinogen: evolutionary conservation of translated and 3'-
 untranslated sequences";
 RL Gene 79:151-158(1989).
 RN [5]
 RP SEQUENCE OF 425-479 FROM N.A.
 RX STRAIN=Wistar; Tissue=Liver;
 MEDLINE=87134033; PubMed=3817019;
 RA Sobczak J., Lotti A.-M., Taroux P., Duguet M.;
 RT "Molecular cloning of mRNA sequences transiently induced during rat
 liver regeneration";
 RL Exp. Cell Res. 169:47-56(1987).
 CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
 polymerize into fibrin and acting as a cofactor in platelet
 aggregation.
 CC -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
 (alpha, beta and gamma), linked to each other by disulfide bonds.
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 which cleaves fibrinopeptides A and B from alpha and beta chains,
 and thus exposes the N-terminal polymerization sites responsible
 for the formation of the soft clot.
 CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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 CC
 DR EMBL; U05675; AAA64866.1; -;
 DR EMBL; M27220; AAA41160.1; -;
 DR EMBL; K01336; AAA98625.1; -;
 DR EMBL; M35602; AAA41159.1; -;
 DR FIB; A05299; A05299.

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DR PIR; I67595; I67595.
DR HSP; P02675; 1FZE.
DR RGD; 2604; Fgb
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
KW Blood coagulation; Direct protein sequencing; Glycoprotein; Plasma;
KW Signal.
FT SIGNAL 1 18
FT CHAIN 19 479 Fibrinogen beta chain.
FT PEPTIDE 19 32 Fibrinopeptide B.
FT DISULFID 211 211 Interchain (with alpha chain) (By
FT 215 215 similarity).
FT DISULFID 215 215 Interchain (with gamma chain) (By
FT 219 304 similarity).
FT DISULFID 219 304 By similarity.
FT DISULFID 229 258 By similarity.
FT DISULFID 412 425 By similarity.
FT CARBOHYD 382 382 N-linked (GlcNAc...) (Potential).
FT CONFLICT 28 30 LSI -> ILS (in Ref. 3).
FT CONFLICT 439 439 L -> Q (in Ref. 5).
FT CONFLICT 441 441 S -> T (in Ref. 5).
FT CONFLICT 445 445 S -> A (in Ref. 5).
FT CONFLICT 467 467 R -> K (in Ref. 5).
FT CONFLICT 475 475 V -> F (in Ref. 5).
SQ SEQUENCE 479 AA; 54303 MW; EC86DB77C3E0EC0 CRC64;

Query Match 85.4%; Score 35; DB 1; Length 479;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 33 GHRPVDR 39
|||||:

RESULT 21
Q8K08 PRELIMINARY; PRT; 481 AA.
ID Q8K08;
AC Q8K08;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fibrinogen, B beta polypeptide.
GN Name=Fgb;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.C., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
```

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031715; AAH31715.1; -.
DR HSP; P02675; 1FZE.
DR MGD; MGI:99501; Fgb.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
SQ SEQUENCE 481 AA; 54752 MW; 9902830CF708A155 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 481;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 35 GHRPVDR 41
|||||:

RESULT 22
Q7TME5 PRELIMINARY; PRT; 503 AA.
ID Q7TME5;
AC Q7TME5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Acl-581 (Acl-216) (Acl-181).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC Xu C.S., Li W.Q., Li Y.C., Chang C.F., Chai L.Q., Yuan J.Y.,
RA Yuan K.J., Yan H.M., Zhao L.F., Ma H., Wang L., Wang S.F., Han H.P.,
RA Wang G.P., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Xu C.S., Li W.Q., Li Y.C., Wang S.F., Han H.P., Wang G.P., Chai L.Q.,
RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC Xu C.S., Li W.Q., Li Y.C., Yang K.J., Yan H.M., Chang C.F., Zhao L.F.,
RA Ma H., Wang L., Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY321323; AAP86255.1; -.
DR EMBL; AY321513; AAP92554.1; -.
DR EMBL; AY321517; AAP92548.1; -.
DR HSP; P02675; 1FZE.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
SQ SEQUENCE 503 AA; 56612 MW; 02B6A1E05E7B5C12 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 503;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 32 GHRPVDR 38
|||||:
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RESULT 23
Q9HA50
ID O9HA50 PRELIMINARY; PRT; 505 AA.
AC O9HA50
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein FLJ12240 (L19).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Oka T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto K., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami J., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oehima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiya H., Satoh N., Takami S., Takashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs";
RL Nat. Genet. 36:40-45(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: AK022302; BAB14006.1; -
DR EMBL: AY598338; AAT06749.1; -
SQ SEQUENCE 505 AA; 54782 MW; 43BADEB48C0DFBE7 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 505;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 41 GHRPLSK 47

RESULT 24
ID Q6P3R6 PRELIMINARY; PRT; 598 AA.
AC Q6P3R6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE KIA00999 protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC063887; AAH63887.1; -
DR EMBL: BC063887; AAH63887.1; -
SQ SEQUENCE 598 AA; 65097 MW; 58754EDC8E547598 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 598;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 194 GHRPLSK 200

RESULT 25
Q641L5
ID Q641L5 PRELIMINARY; PRT; 643 AA.
AC Q641L5
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE BC033915 protein.
GN Name=BC033915;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC063887; AAH63887.1; -
DR EMBL: BC063887; AAH63887.1; -
SQ SEQUENCE 598 AA; 65097 MW; 58754EDC8E547598 CRC64;
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RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC082313; AAH82313.1; -
SQ SEQUENCE 643 AA; 70222 MW; EE66AF7C3AC1310B CRC64;

Query Match 85.4%; Score 35; DB 2; Length 643;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 179 GHRPLSK 185
|||||

RESULT 26
ID Q46583 PRELIMINARY; PRT; 959 AA.
AC Q46583;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DcrH.
GN Name=dcrH;
OS Desulfovibrio vulgaris.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=881;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Hildenborough;
RC MEDLINE=94117369; PubMed=8288529;
RX Deckers H.M., Voordouw G.;
RA "The dcr gene family of Desulfovibrio: implications from the sequence
RT of dcrH and phylogenetic comparison with other mcp genes.";
RL Antonie Van Leeuwenhoek 70:21-29(1996).
DR EMBL; U30319; AAB50497.1; -
DR PIR; H36943; H36943.
DR HSSP; P02942; 1QU7.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004089; Chmtaxis.trans.
DR InterPro; IPR002063; Hemerythrin.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF01814; Hemerythrin; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR ProDom; PD006099; Hemerythrin; 1.
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DR SMART; SM00304; HAMP; 1.
DR SMART; SM00283; MA; 1.
DR PROSITE; PS0111; CHEMOTAXIS_TRANSLOC_2; 1.
DR PROSITE; PS00885; HAMP; 1.
DR PROSITE; PS00550; HEMERYTHRINS; UNKNOWN 1.
SQ SEQUENCE 959 AA; 104728 MW; 450550E840954D42 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 959;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
DB 513 HRPLDK 518
|||||

RESULT 27
ID Q6ZQ09 PRELIMINARY; PRT; 1052 AA.
AC Q6ZQ09;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKIAA0999 protein (fragment).
GN Name=MKIAA0999;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP PubMed=14621295;
RX Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129257; BAC98067.1; -
DR InterPro; IPR000449; UBA.
DR InterPro; IPR009060; UBA like.
DR PROSITE; PS50030; UBA; 1.
FT NON TER 1 1
SQ SEQUENCE 1052 AA; 115918 MW; 6DE5F456329E21A4 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 1052;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 588 GHRPLSK 594
|||||

RESULT 28
ID Q6P4S6 PRELIMINARY; PRT; 1311 AA.
AC Q6P4S6; Q66JZ5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CDNA sequence BC033915.
GN Name=BC033915;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=FVB/N; TISSUE=Limb, and Salivary gland;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones J.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC SEQUENCE FROM N.A.
RP STRAIN=FVB/N; TISSUE=Salivary gland;
RA Director MGC Project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC063268; AAH63268.2; -.
DR EMBL; BC080688; AAH80688.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR008271; Ser Thr pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1311 AA; 145810 MW; CF11B8995BC3F2B CRC64;

Query Match 85.4%; Score 35; DB 2; Length 1311;
Best Local Similarity 85.7%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 847 GHRPLSK 853

RESULT 29
Q6CH64
ID Q6CH64 PRELIMINARY; PRT; 1345 AA.
AC Q6CH64;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P13433 Saccharomyces cerevisiae DNA-directed RNA
DE Polymerase.
GN ORFNames=YAL10A12001g;

OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Lafontaine I., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Dufon B., de Montigny J., March C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates (By similarity).
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -1- SIMILARITY: Belongs to the phage and mitochondrial RNA polymerase
CC family.
DR EMBL; CR382127; CAG83927.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR009050; Globin_like.
DR InterPro; IPR002092; RNA_pol_phage.
DR Pfam; PF0940; RNA_pol; 1.
DR PROSITE; PS00900; RNA_POL_PHAGE 1; 1.
DR PROSITE; PS00489; RNA_POL_PHAGE 2; 1.
KW DNA-directed RNA polymerase; Transcription; Transferase.
SQ SEQUENCE 1345 AA; 152077 MW; D2A7B91A9F970244 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 1345;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
| | | | |
Db 1281 HRPLDK 1286

RESULT 30
Q9Y2K2
ID Q9Y2K2 PRELIMINARY; PRT; 1371 AA.
AC Q9Y2K2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIAA0999 protein (Fragment).
GN Name=KIAA0999;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

RX MEDLINE=99246063; PubMed=10231032;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:63-70(1999).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB023216; BAA76843.2; -.
DR HSSP; P49137; INY3.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011008; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR000449; UBA.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 1371 AA; 149525 MW; F0FBA385B8226158 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 1371;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 907 GHRPLSK 913
|||||

RESULT 31
MUA2_THETN STANDARD; PRT; 417 AA.
ID Q8R9G7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2 (EC 2.5.1.7)
DE (Enolpyruvate transferase 2) (UDP-N-acetylglucosamine enolpyruvyl
DE transferase 2) (EPT 2).
GN Name=murA2; OrderedLocusNames=TTE1644;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11973336; DOI=10.1101/gr.219302;
RA Bao O., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
CC -1- FUNCTION: Cell wall formation. Adds enolpyruvyl to UDP-N-
CC acetylglucosamine (By similarity).
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + UDP-N-acetyl-D-
CC glucosamine = phosphate + UDP-N-acetyl-3-O-(1-carboxyvinyl)-D-
CC glucosamine.
CC -1- PATHWAY: Peptidoglycan biosynthesis; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the EPSP synthase family. MurA subfamily.

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CC or send an email to license@isb-sib.ch).

DR EMBL; AE013119; AAM24846.1; -.
DR HSSP; P33038; IDLG; 1.
DR HAMAP; MF_00111; -; 1.
DR InterPro; IPR005750; AcGlu_Tran_Mura.
DR InterPro; IPR001986; EPSP synth.
DR Pfam; PF00275; EPSP synthase; 1.
DR ProDom; PD001867; EPSP synth; 1.
DR TIGRPFAMs; TIGR01072; mura; 1.
KW Cell division; Cell wall; Complete proteome; Peptidoglycan synthesis;
KW Transferase.
FT ACT_SITE 116 116 Proton donor (By similarity).
FT BINDING 116 116 PEP (covalent) (By similarity).
SQ SEQUENCE 417 AA; 45211 MW; 0A199EC2B104DC6E CRC64;

Query Match 82.9%; Score 34; DB 1; Length 417;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
DB 119 GHRPID 124
|||||

RESULT 32
Q67J65 PRELIMINARY; PRT; 424 AA.
ID Q67J65;
AC Q67J65;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE UDP-N-acetylglucosamine enolpyruvyl transferase.
GN ORFNames=STH3304;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IAM14863;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Complete genome sequence of an uncultured bacterium Symbiobacterium
RT thermophilum.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006840; BAD42285.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR005750; AcGlu_Tran_Mura.
DR InterPro; IPR001986; EPSP synth.
DR Pfam; PF00275; EPSP synthase; 1.
DR ProDom; PD001867; EPSP synth; 1.
DR TIGRPFAMs; TIGR01072; mura; 1.
KW Transferase.
SQ SEQUENCE 424 AA; 45497 MW; 004C2B0B0C064DAA CRC64;

Query Match 82.9%; Score 34; DB 2; Length 424;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 121 GHRPVDQ 127
|||||

RESULT 33
Q7S2E9 PRELIMINARY; PRT; 426 AA.
ID Q7S2E9
AC Q7S2E9;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Predicted protein.
 GN Name=NCU06008.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gherre S.,
 RA Kamal M., Kamysseis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
 RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
 RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 RA Varden O., Planann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Eboile D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
 RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
 RL Nature 0:0-0(2003).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; ABX01000426; EAA29580.1; -.
 SQ SEQUENCE 426 AA; 48541 MW; 8D93CB4C4625B926 CRC64;

 Query Match 82.9%; Score 34; DB 2; Length 426;
 Best Local Similarity 71.4%; Pred.No. 2.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 1 GHRPLDK 7
 DB 97 GHQPLDR 103

 RESULT 34
 ID Q751V1 PRELIMINARY; PRT; 440 AA.
 AC Q751V1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE AFR724CP.
 GN Name=AFR724C;
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715; DOI=10.1126/science.1095781;
 RA Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
 RA Gaffney T.D., Philippsen P.;
 RA "The Ashbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome.";
 RL Science 304:304-307(2004).
 DR EMBL; AS016904; AAS54096.1; -.
 DR AGD; AFR724C; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004648; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase_like.

DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TYKIC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding.
 SQ SEQUENCE 440 AA; 50173 MW; AA3E5A17E4904118 CRC64;

 Query Match 82.9%; Score 34; DB 2; Length 440;
 Best Local Similarity 85.7%; Pred.No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 GHRPLDK 7
 DB 215 GHPLDK 221

 RESULT 35
 ID Q94271 PRELIMINARY; PRT; 673 AA.
 AC Q94271;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE SPBP8B7.23 protein.
 GN Name=SPBP8B7.23;
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972h-;
 RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odel C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Welljens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S.,
 RA Gabell C., Fuchs M., Dusterhoft A., Fritz C., Holzer E., Moestl D.,
 RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
 RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RA "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL; AL032684; CAA21808.1; -.
 DR PIR; T40817; T40817.
 DR GeneDB Spombe; SPBP8B7.23; -.
 DR GO; GO:0000153; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.

DR GO: 0016567; P:protein ubiquitination; IEA.
 DR InterPro: IPR001841; Znf ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 673 AA; 76459 MW; 7317BDAD768FC883 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 673;
 Best Local Similarity 71.4%; Pred. No. 3.4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 |||||
 Db 160 GHRPMDK 166

RESULT 36

Q9S1Z7 PRELIMINARY; PRT; 795 AA.
 AC Q9S1Z7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein At2g22020.
 GN Name:At2g22020;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 [1]
 RN SEQUENCE FROM N.A.
 RP Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
 RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
 RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
 RA Fraser C.M., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Town C.D., Kaul S.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: ACO07019; AAD20419.1; -
 DR FIR; A84608; A84608.
 DR InterPro: IPR003877; SPRY_receptor.
 DR Pfam: PF00622; SPRY; 1.
 DR SMART: SM00449; SPRY; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 795 AA; 89006 MW; 07625DE69DBBPEOD CRC64;

Query Match 82.9%; Score 34; DB 2; Length 795;
 Best Local Similarity 71.4%; Pred. No. 4.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 |||||
 Db 41 GHRPLER 47

RESULT 37

Q6C3A7 PRELIMINARY; PRT; 844 AA.
 AC Q6C3A7;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to sp|F31244 Saccharomyces cerevisiae DNA repair protein RAD16.
 DE RAD16.
 GN ORFNames=YAL10F01232g;
 OS Yarrowia lipolytica CLIB99.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.

OX NCBI_TaxID=284591;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CLIB99;
 RC Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talia E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikoleki M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Sennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CLIB99;
 RC Genoscope;
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RL -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC EMBL: CR382132; CAG77657.1; -
 DR GO: 0000151; C:ubiquitin ligase complex; IEA.
 DR GO: 0005524; F:ATP binding; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR GO: 0004386; F:helicase activity; IEA.
 DR GO: 0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: 0008270; F:zinc ion binding; IEA.
 DR GO: 0016567; P:protein ubiquitination; IEA.
 DR InterPro: IPR011545; DEAD/DEAH_N.
 DR InterPro: IPR002464; DEAD_box.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR00330; SNF2_N.
 DR InterPro: IPR01841; Znf_Ring.
 DR Pfam: PF00271; Helicase_C; 1.
 DR Pfam: PF00176; SNF2_N; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00690; DEAD ATP HELICASE; UNKNOWN_1.
 DR PROSITE: PS00518; ZF_RING_1; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 844 AA; 95270 MW; 055B25AB3563A1CF CRC64;

Query Match 82.9%; Score 34; DB 2; Length 844;
 Best Local Similarity 83.3%; Pred. No. 4.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
 |||||
 Db 459 GHRPMD 464

RESULT 38

Q94MW0 PRELIMINARY; PRT; 67 AA.
 ID Q94MW0;
 AC Q94MW0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ORF soc.2.
 DE ORF soc.2.
 GN Name=soc.2;
 OS Bacteriophage T6.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC T4-like viruses.

```
OX NCBI_TaxID=10666;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21353060; PubMed=11459968; DOI=10.1073/pnas.131007398;
RA Mosig G., Gwin J., Luder A., Colowick N., Vo D.;
RT "Two recombination-dependent DNA replication pathways of bacteriophage
RT T4, and their roles in mutagenesis and horizontal gene transfer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8306-8311(2001).
DR EMBL; AF374620; AAK66984.1; -.
SQ SEQUENCE 67 AA; 8010 MW; D8C5AA794200D0A6 CRC64;

Query Match      80.5%; Score 33; DB 2; Length 67;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 46 GHIPLDK 52

RESULT 39
Q89KQ4
ID Q89KQ4 PRELIMINARY; PRT; 107 AA.
AC Q89KQ4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE BLr4850 protein.
GN OrderedLocusNames=blr4850;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005952; BAC50115.1; -.
KW Complete proteome.
SQ SEQUENCE 107 AA; 11691 MW; 6F84E6EC42927A11 CRC64;

Query Match      80.5%; Score 33; DB 2; Length 107;
Best Local Similarity 83.3%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 26 GHRPVD 31

RESULT 40
Q8ILT7
ID Q8ILT7 PRELIMINARY; PRT; 146 AA.
AC Q8ILT7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PF14_0157;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
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RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shalloo S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McPadden G.I., Cummings L.M., Subramanian G.M., Mungall C., R.W.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014818; AAN38769.1; -.
KW Hypothetical protein.
SQ SEQUENCE 146 AA; 16861 MW; D8C846512C2379D2 CRC64;

Query Match      80.5%; Score 33; DB 2; Length 146;
Best Local Similarity 85.7%; Pred. No. 11e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 2 GHRPLDK 8
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Search completed: June 1, 2005, 11:51:59
Job time : 108 secs